FIG. 1A

```
                                                             GGCTGCCGG
                                                                  -120
AGGGGCGGCCGTGCGTGGATGCGGCGGGAGCTGGAAGCCTCGAGCAGCCGGCGCCTTCT

CTGGCCCCGGGCGCCATATGGCTTGAAGAGCCGTGCCACCCAGTGGCCCCACTGCCCCA
                                                                    -1
 1              *                       10
Met Asp Pro Leu Asn Leu Ser Trp Tyr Asp Asp Asp Leu Glu Arg
ATG GAT CCA CTG AAC CTG TCC TGG TAC GAT GAC GAT CTG GAG AGG
1
     *          20          *                              30
Gln Asn Trp Ser Arg Pro Phe Asn Gly Ser Glu Gly Lys Ala Asp
CAG AAC TGG AGC CGG CCC TTC AAT GGG TCA GAA GGG AAG GCA GAC
                                                            90
                                        40
Arg Pro His Tyr Asn Tyr Tyr Ala Met Leu Leu Thr Leu Leu Ile
AGG CCC CAC TAC AAC TAC TAT GCC ATG CTG CTC ACC CTC CTC ATC

                50                                         60
Phe Ile Ile Val Phe Gly Asn Val Leu Val Cys Met Ala Val Ser
TTT ATC ATC GTC TTT GGC AAT GTG CTG GTG TGC ATG GCT GTA TCC
                                                           180
```

#3

```
                                             70
Arg Glu Lys Ala Leu Gln Thr Thr Thr Asn Tyr Leu Ile Val Ser
GCA GAG AAG GCT TTG CAG ACC ACC ACC AAC TAC TTG ATA GTC AGC

                    80                                   90
Leu Ala Val Ala Asp Leu Leu Val Ala Thr Leu Val Met Pro Trp
CTT GCT GTG GCT GAT CTT CTG GTG GCC ACA CTG GTA ATG CCG TGG
                                                        270
                                        100
Val Val Tyr Leu Glu Val Val Gly Glu Trp Lys Phe Ser Arg Ile
GTT GTC TAC CTG GAG GTG GTG GGT GAG TGG AAA TTC AGC AGG ATT

                    110                                 120
His Cys Asp Ile Phe Val Thr Leu Asp Val Met Met Cys Thr Ala
CAC TGT GAC ATC TTT GTC ACT CTG GAT GTC ATG ATG TGC ACA GCA
                                                        360
                                        130
Ser Ile Leu Asn Leu Cys Ala Ile Ser Ile Asp Arg Tyr Thr Ala
AGC ATC CTG AAC CTG TGT GCC ATC AGC ATT GAC AGG TAC ACA GCT

                    140                                 150
Val Ala Met Pro Met Leu Tyr Asn Thr Arg Tyr Ser Ser Lys Arg
GTG GCA ATG CCC ATG CTG TAT AAC ACA CGC TAC AGC TCC AAG CGC
                                                        450
```

FIG. 1B

```
                                             160
Arg Val Thr Val Met Ile Ala Ile Val Trp Val Leu Ser Phe Thr
CGA GTT ACT GTC ATG ATT GCC ATT GTC TGG GTC CTG TCC TTC ACC

                170                                     180
Ile Ser Cys Pro Leu Leu Phe Gly Leu Asn Asn Thr Asp Gln Asn
ATC TCC TGC CCA CTG CTC TTC GGA CTC AAC AAT ACA GAC CAG AAT
                                                        540
                                     190
Glu Cys Ile Ile Ala Asn Pro Ala Phe Val Val Tyr Ser Ser Ile
GAG TGT ATC ATT GCC AAC CCT GCC TTT GTG GTC TAC TCC TCC ATT

                200                                     210
Val Ser Phe Tyr Val Pro Phe Ile Val Thr Leu Leu Val Tyr Ile
GTC TCA TTC TAC GTG CCC TTC ATC GTC ACT CTG CTG GTC TAT ATC
                                                        630
                                     220
Lys Ile Tyr Ile Val Leu Arg Lys Arg Arg Lys Arg Val Asn Thr
AAA ATC TAC ATC GTC CTC CGG AAG CGC CGG AAG CGG GTC AAC ACC

                230                                     240
Lys Arg Ser Ser Arg Ala Phe Arg Ala Asn Leu Lys Thr Pro Leu
AAG CGC AGC AGT CGA GCT TTC AGA GCC AAC CTG AAG ACA CCA CTC
                                                        720
```

FIG. 1C

```
                                                      250
Lys Asp Ala Ala Arg Arg Ala Gln Glu Leu Glu Met Glu Met Leu
AAG GAT GCT GCC CGC CGA GCT CAG GAG CTG GAA ATG GAG ATG CTG

                260
Ser Ser Thr Ser Pro Pro Glu Arg Thr Arg Tyr Ser Pro Ile 270
TCA AGC ACC AGC CCC CCA GAG AGG ACC CGG TAT AGC CCC ATC Pro
                                                        CCT
                                                        810
                                      280
Pro Ser His His Gln Leu Thr Leu Pro Asp Pro Ser His His Gly
CCC AGT CAC CAC CAG CTC ACT CTC CCT GAT CCA TCC CAC CAC GGC

                290
Leu His Ser Asn Pro Asp Ser Pro Ala Lys Pro Gly Lys Asn 300
CTA CAT AGC AAC CCT GAC AGT CCT GCC AAA CCA GAG AAG AAT Gly
                                                        GGG
                                                        900
                                      310
His Ala Lys Ile Val Asn Pro Arg Ile Ala Lys Phe Phe Glu Ile
CAC GCC AAG ATT GTC AAT CCC AGG ATT GCC AAG TTC TTT GAG ATC

                320
Gln Thr Met Pro Asn Gly Lys Thr Arg Thr Ser Leu Lys Thr 330
CAG ACC ATG CCC AAT GGC AAA ACC CGG ACC TCC CTT AAG ACG Met
                                                        ATG
                                                        990
```

FIG. 1D

```
                                   340
Ser Arg Arg Lys Leu Ser Gln Gln Lys Glu Lys Lys Ala Thr Gln
AGC CGC AGA AAG CTC TCC CAG CAG AAG GAG AAG AAA GCC ACT CAG

                350                                         360
Met Leu Ala Ile Val Leu Gly Val Phe Ile Ile Cys Trp Leu Pro
ATG CTT GCC ATT GTT CTC GGT GTG TTC ATC ATC TGC TGG CTG CCC
                                                           1080
                                   370
Phe Phe Ile Thr His Ile Leu Asn Ile His Cys Asp Cys Asn Ile
TTC TTC ATC ACG CAC ATC CTG AAT ATA CAC TGT GAT TGC AAC ATC

                380                                         390
Pro Pro Val Leu Tyr Ser Ala Phe Thr Trp Leu Gly Tyr Val Asn
CCA CCA GTC CTC TAC AGC GCC TTC ACA TGG CTG GGC TAT GTC AAC
                                                           1170
                                   400
Ser Ala Val Asn Pro Ile Ile Tyr Thr Thr Phe Asn Ile Glu Phe
AGT GCC GTC AAC CCC ATC ATC TAC ACC ACC TTC AAC ATC GAG TTC

                410                415
Arg Lys Ala Phe Met Lys Ile Leu His Cys
CGC AAG GCC TTC ATG AAG ATC TTG CAC TGC TGAGTCTGCCCCTTGCCTG
                                                           1264
```

FIG. 1E

CACAGCAGCTGCTTCCCACCTCCCTGCCTATGCAGGCCAGACCTCATCCCTGCAAGCTG

TGGGCAGAAAGGCCCAGATGAACTTGGCCTTCTCTCGACCCTGCAGGCCCTGCAGTGTTA 1383

GCTTGGCTCGATGCCCCTCTCTGCCCACACACCCTCATCCTGCCAGGGTAGGGCCAGGG

AGACTGGTATCTTACCAGCTCTGGGGTTGGACCCATGGCTCAGGGCAGCTCACAGAGTGC 1502

CCCTCTCATATCCAGACCCTGTCTCCTTGGCACCAAAGATGCAGCGGCCTTCCTTGACC

TTCCTCTTGGGCACAGAAACTAGCTCAGTGGTCGAGCACACCCTGATCGCTGGCTTGGCC 1621

TGGCCCTTGCTTGCCTGTGCCGGATCAGGTGGTGGGAGGGAGCGACACGTTCTTACTTT

ATAGGAACCACATAGGAAAGCAGGGAACACGCCAAGTCCTCCAGGCACATCAGTGTCAGG 1740

AGACACACATAAACACCAGGTAGCTCCATGGACCCCAGAGAAACTGAGGCTGAAAAATC

TGTTTTCCACTCCAACTCTAGTGTGAGTCCCTACTTTTCATAGCCATGGGTATTACTATG 1859

FIG. 1F

TCCTACCTTGTTATAGTATCCCATGGGGTTTCTGTACCATTTGGGGGAAAACAACTCTA

ATCCTCAAGGGCCCCAAGAGAATCTGTAAGGAGAAAAATAGGCTGATCTCCCTCTACTCT
1978

CCAATCCACTCCACCACTTCTTGATATACCTTGGATGTATCCATTCCTCACAGCAAATG

CTGGCCAGTCAGGCCTTGGACCAGTGTTGGAGTTGAAGCTGGATGTGGTAACTTGGGGCT
2097

CTTTGGGGCTGGGGGGGTTGTTAACATCGTCTCTCTTCCATATCTCTTCCTTCCCAGTG

CCTCTGCCTTAGAAGAGGCTGTGGATGGGGTGCTGGGACTGCTGATACCATTGGGCCTGG
2216

CCCTGAATGAGGAGGGGAAGCTGCAGTTTGGAGGGTTCTGGGATCCAACTCTGTAACAT

CACTATACCTGTACCAAAACTAATAAAACCTTGACAAGAGTCAAAAAAAAAAA
2317

FIG. 1G

```
                                                              I
Dδ    MD....PL...NISWYDDDLERQNWSRPFNGSEGKADRPHYNYYAMIITLL.IFIIVFGNVLVCMAVSREKALQTITNY
βδ    MGP...P...GNDSDFLLTTNGSHV...PDHDVTEERDEAWVVGMAIIMSVIVLAIVFGNVLVITAIAKFERLQTVTNY
αδ    MGSLQ.PQA.GNASWNGTEAPG..GGARATPYSLQVT....LTLVCLAGLL.MLLTVFGNVLVIIAVFTSRAIKAPQNL
G-21  MDVLS.PGQ.QNNTTSPPAPFE..TGGNTTGISDVTVSYQV.ITSLIIGTL.IFCAVIGNACVVAAIALERSLQNVANY
M1    MNTSAPPAVSPNITVLAP.....GKGPWQVA...........FIGITTGLL.SLATVIGNILVIISFKVNTELKTVNNY
SK    MGACV.VMTDINIS.......SGLDSNATGITAFSMPGWQLALWTAAYLAL.VLVAVMGNATVIWIILAHQRMRIVTNY

              II                                  III
Dδ    LIVSLAMADIIVATLVMPWVVYLEVVGEWKFSRIHCDIFVTLDVMMCTASILNLCAISIQRYTAVAMPMIYMTRYSSKRR
βδ    FILDSLACADLVMGIAVVPFGASHIIMKMWNFGNFWCEFWTSIQVLCVTASIETLCVIAVQRYIAITSPFKYQSLLTKNKA
αδ    FIVSLASADILVATLVIPFSLANEVMQYWYFGKTWCEIYLALDVLFCTSSIVHLCAISIQRYWSITQAIEYNLKRTPRRI
G-21  LIGSLAVTDIMVSVLVIPMAALYQVLNNWTLGQVTCDLFIALDVLOCTSSILHLCAIAIQRYWAITDPIDYVNKRTPRPR
M1    FLLSLACADLIIGIFSMNLYTTYLLMQIWALGTLACDLWLALDYVASNASVMNLLIISFQRYFSVTRPLSYRAKTRPRRA
SK    FIVNLALADICMAAFNAAFNFVYASHNIWYFGRAFCYFQNLFPITAMFVSIYSMTAIAAQRYMAIVRPFQPRLSAPGTR.

             IV                                        V
Dδ    VTVMIAIVWVISFTISC.PLLFGLNNTD.........QNECIIANPAFVVYSSIMSFYVPFIVTLLVYIKIYIVLRKRRKRVNTKR-(111)
βδ    RMV.ILMVWIVSGLTSFIPIQMHWYRATH..QKAIDCYHRETCCDFFTNQAYAIWSSIVSFYVPLVVMVFVYSRVFQVAKRQLQKI-(32)-
αδ    KAI.LITVWVISAVISFPPLISIEKKGGG....GGPQPAEPRCEINDQKWYVISSCIGSFFAPQLIMILVYVRIYQIAKRRTRVP-(137)
G-21  ALT.SLT.WLIGFLISIPPMLGWRTPEDR.........SDPDACTISKDMGYTIYSTFGAFYIPLLLMLVLYGRIFRAARFRIPKT-(110)
M1    ALM.IGLAWLVSFVLWA.PAILFWQYLVGE....RTVLAGQCYIQFLSQPIITFGTAMAAFYLPVTVMCTLYWRIYRETENRAREL-(137)
SK    .AV.IAGIWLVALALAF.PQCFYSTITTDEGATKCVVAWPEDSGGKMLLLYHLIVIALIYF.LPLVVMFVAYSVIGLTLWRRSVPG-(12)-

                 VI                                  VII
Dδ    -KEKKATQMIAIVIGMFIICWLPFFITHIINIHCQCN....IPPVLYSAFTWLGYVNSA..VNPIIYTTFNIEFRNAFMKILHC
βδ    -KEHKALKTIGIIMGIFTLCWLPFFIVNIVHVIQDNL....IPKEVYILLNWLGYVNSA..PNPIIYCRSP.DFRIAFQEIL.CL--(36)
αδ    -REKRFTFVIAVVIGMFVVCWFPFFFTYTLTAVGCS.....VPRTILFKFFPWPGYCNSS..LNPVIYTLFNHDFRRAFWKIL.CRC--(6)
G-21  -RERKTVKTLQIIMGIFILCWLPFFIVALVLPPCESSC..HMPTILGAIINWLGYSNSL..INPVLYAYFNKDFQNAFWKIIKCNFCRQ
M1    -KEKKAARTLSAILLAFIVTWT YNIMVLVSTFCKDC...VPETIWELGYWIGYVNST..LNPMCYALQNKAFRDTFRLLLHCR--(24)
SK    -AKKKFVKTMVIVVVTFAICWLPYHLYFIIGTFQEDIYCHKFIQQVYLALPWIA..MSSTMYNPIIYCCINHRFRSQFRLAPRCC--(62)
```

FIG. 2

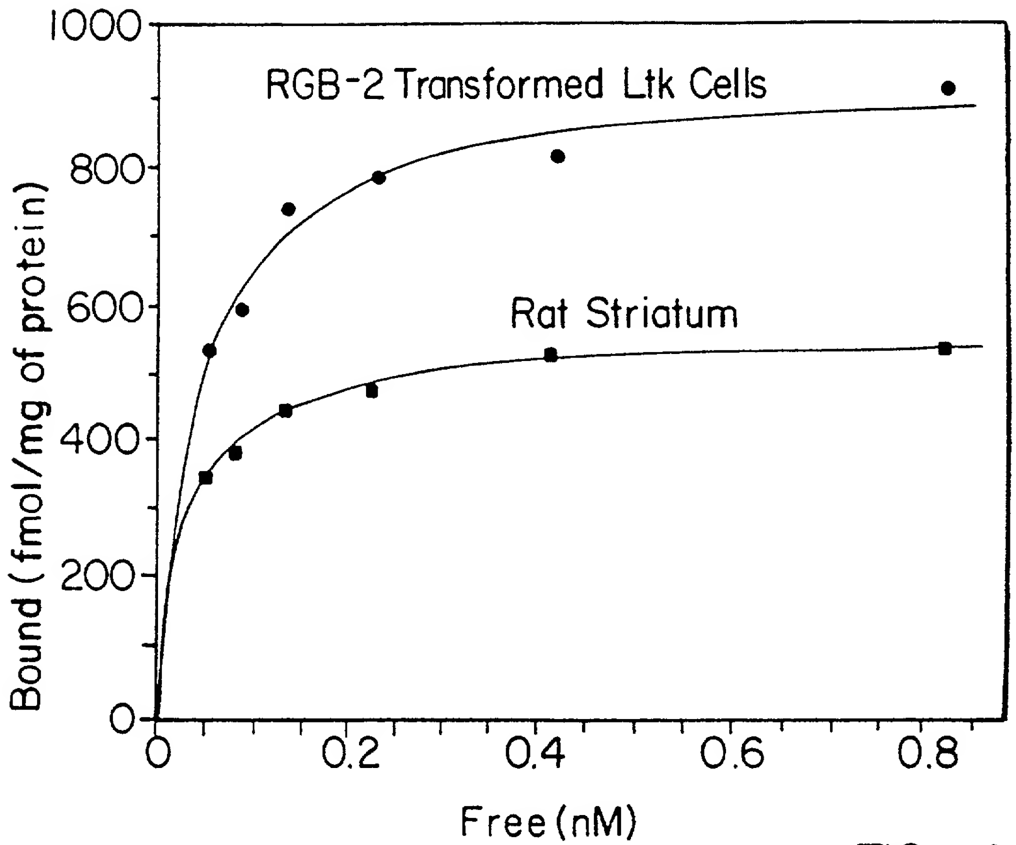


FIG.4A-1

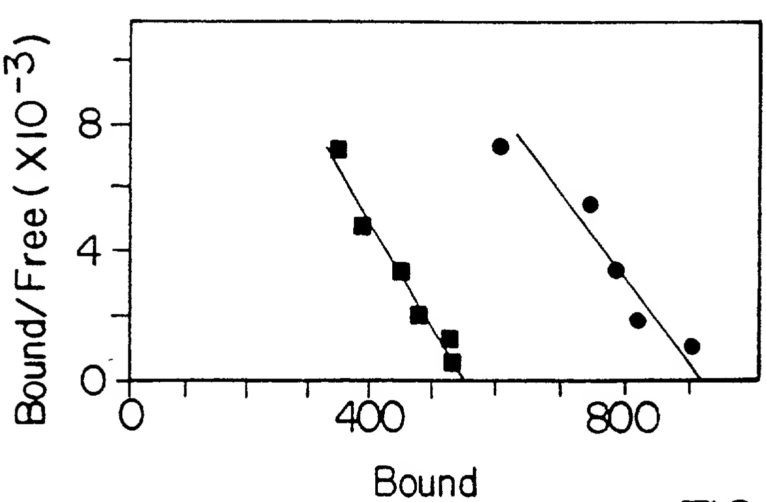
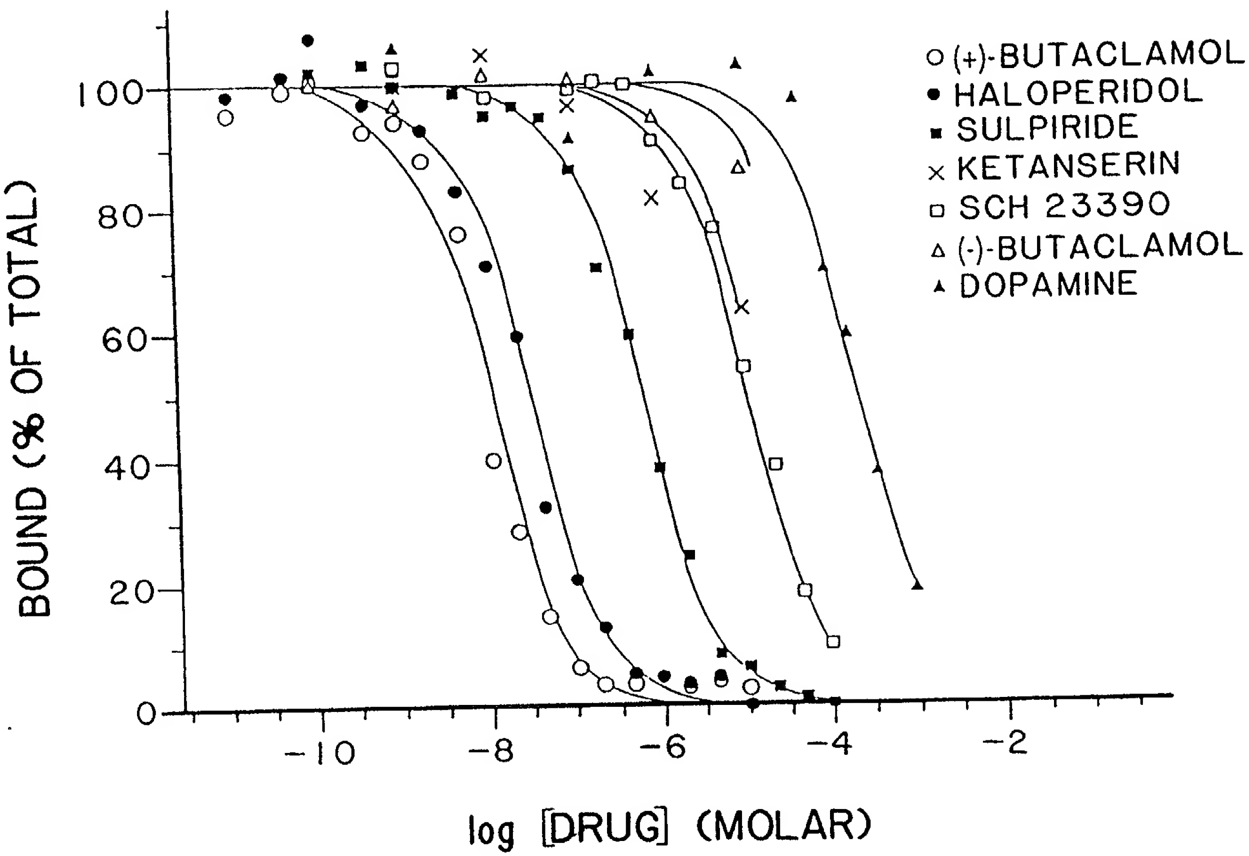


FIG.4A-2

FIG. 4B



(+)-BUTACLAMOL
HALOPERIDOL
SULPIRIDE
KETANSERIN
SCH 23390
(-)-BUTACLAMOL
DOPAMINE
BOUND (% OF TOTAL)
100
80
60
40
20
0
-10
-8
-6
-4
-2
log [DRUG] (MOLAR)

DRUG	Ki (nM)		
	RGB-2		
	Transformed Ltk-Cells	Rat Striatum	
(+)-Butaclamol	0.83	1.0	
(-)-Butaclamol	>1,000	>1,000	
Haloperidol	3.0	5.3	
Dopamine + GTP	17,000	6,300	
Sulpiride			
high affinity	80	67	(87%)
low affinity	---	>10,000	(13%)
SCH 23390			
high affinity	---	35	(16%)
low affinity	1,000	780	(84%)
Ketanserin			
high affinity	---	27	(25%)
low affinity	>1,000	>1,000	(75%)

FIG. 4C

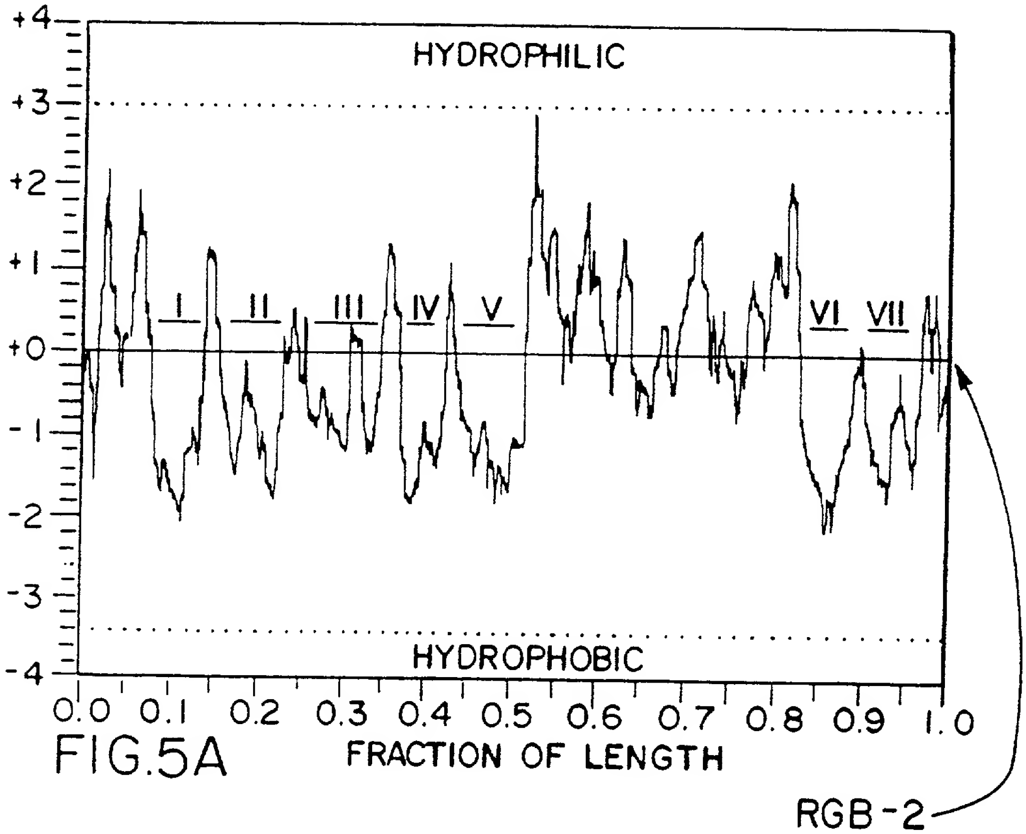

HYDROPHILIC
HYDROPHOBIC
+4
+3
+2
+1
+0
-1
-2
-3
-4
I
II
III
IV
V
VI
VII
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
FRACTION OF LENGTH
RGB-2

FIG.5A

FIG.5B

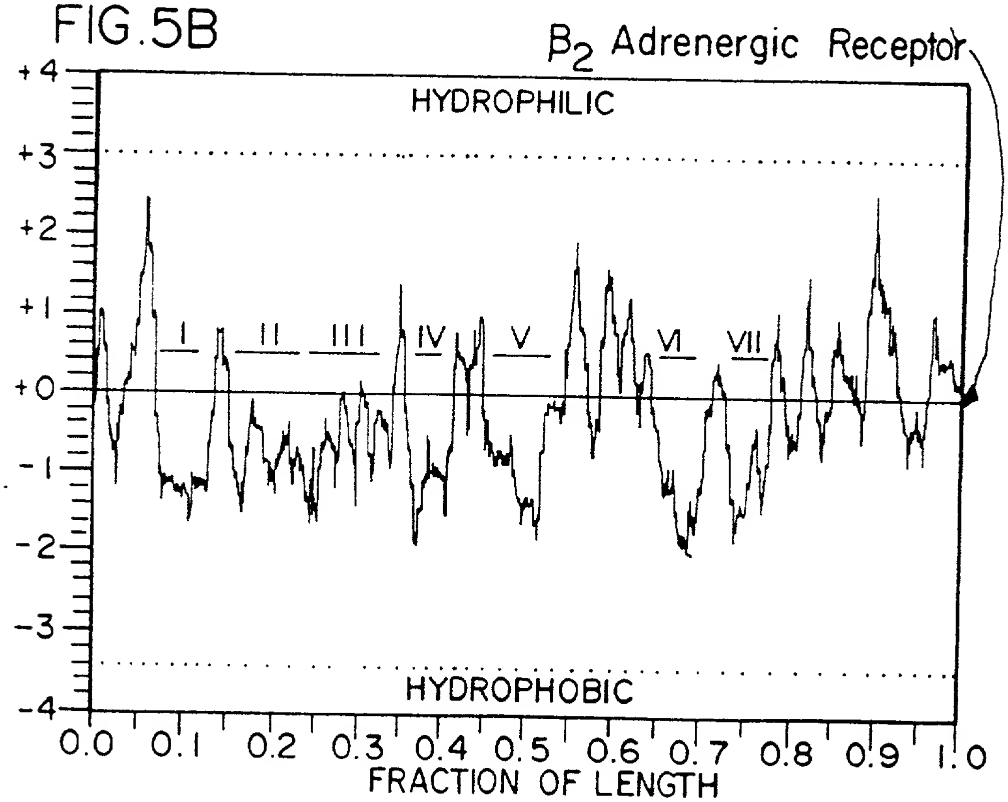
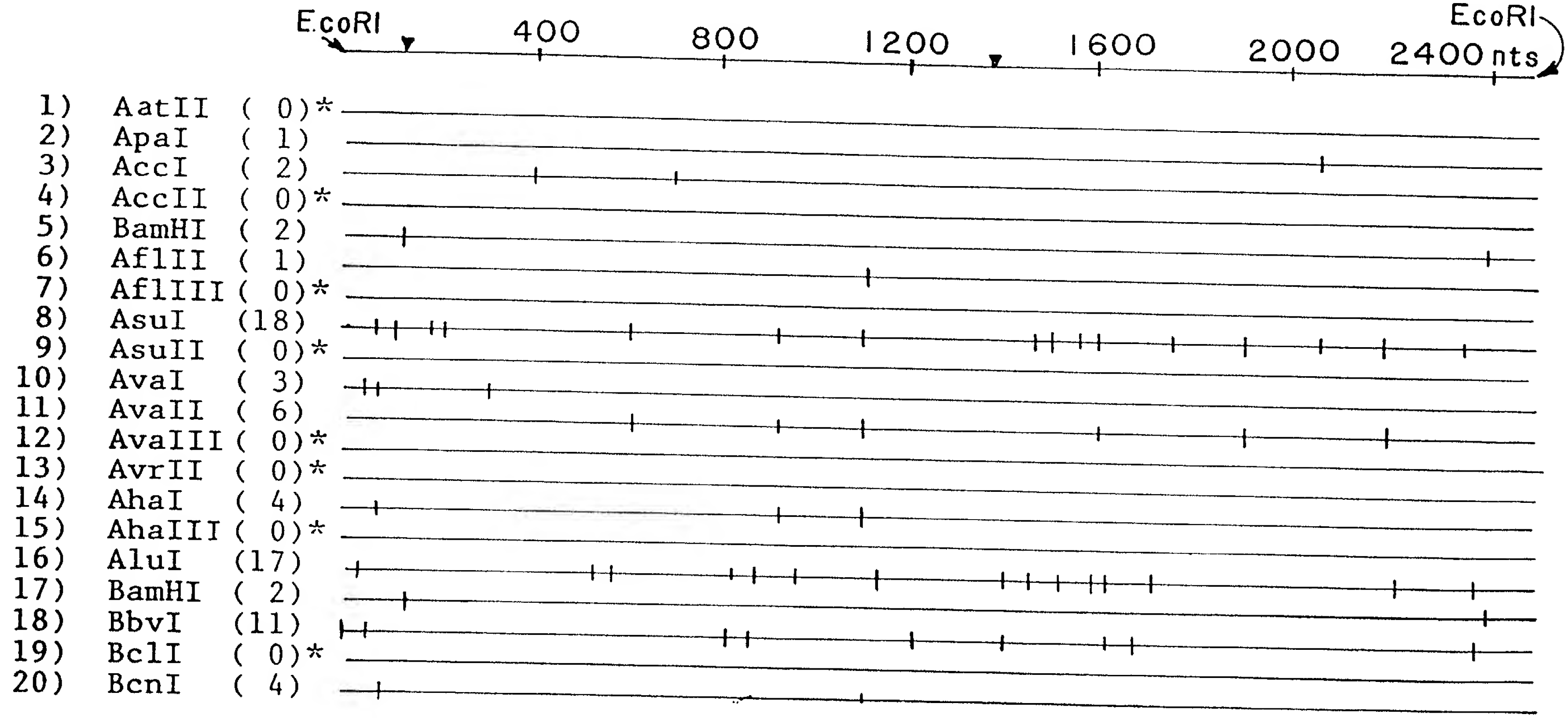
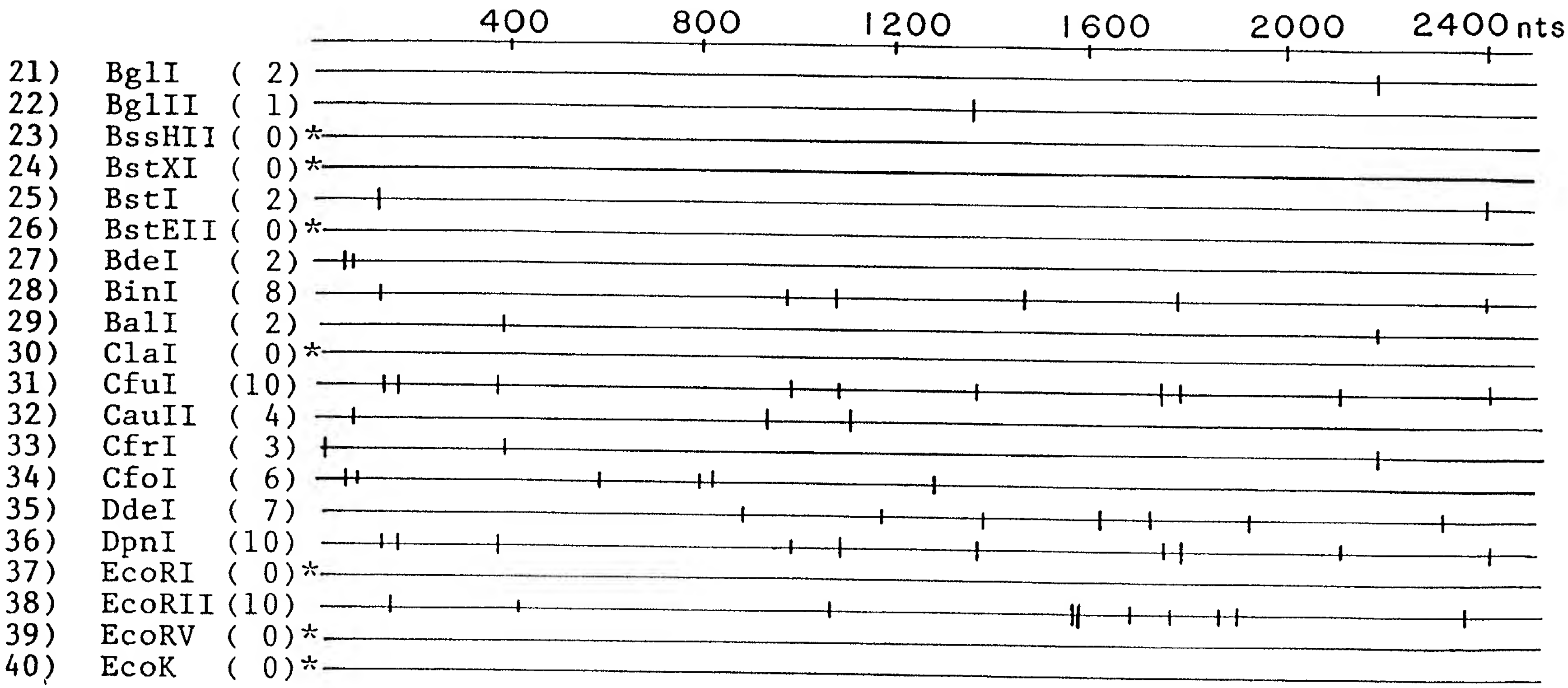

β_2 Adrenergic Receptor
HYDROPHILIC
HYDROPHOBIC
+4
+3
+2
+1
+0
-1
-2
-3
-4
I
II
III
IV
V
VI
VII
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
FRACTION OF LENGTH

FIG. 6A

Length of DNA: 2477 nts





400
800
1200
1600
2000
2400 nts
21) BglI (2)
22) BglII (1)
23) BssHII (0)*
24) BstXI (0)*
25) BstI (2)
26) BstEII (0)*
27) BdeI (2)
28) BinI (8)
29) BalI (2)
30) ClaI (0)*
31) CfuI (10)
32) CauII (4)
33) CfrI (3)
34) CfoI (6)
35) DdeI (7)
36) DpnI (10)
37) EcoRI (0)*
38) EcoRII (10)
39) EcoRV (0)*
40) EcoK (0)*

FIG. 6B

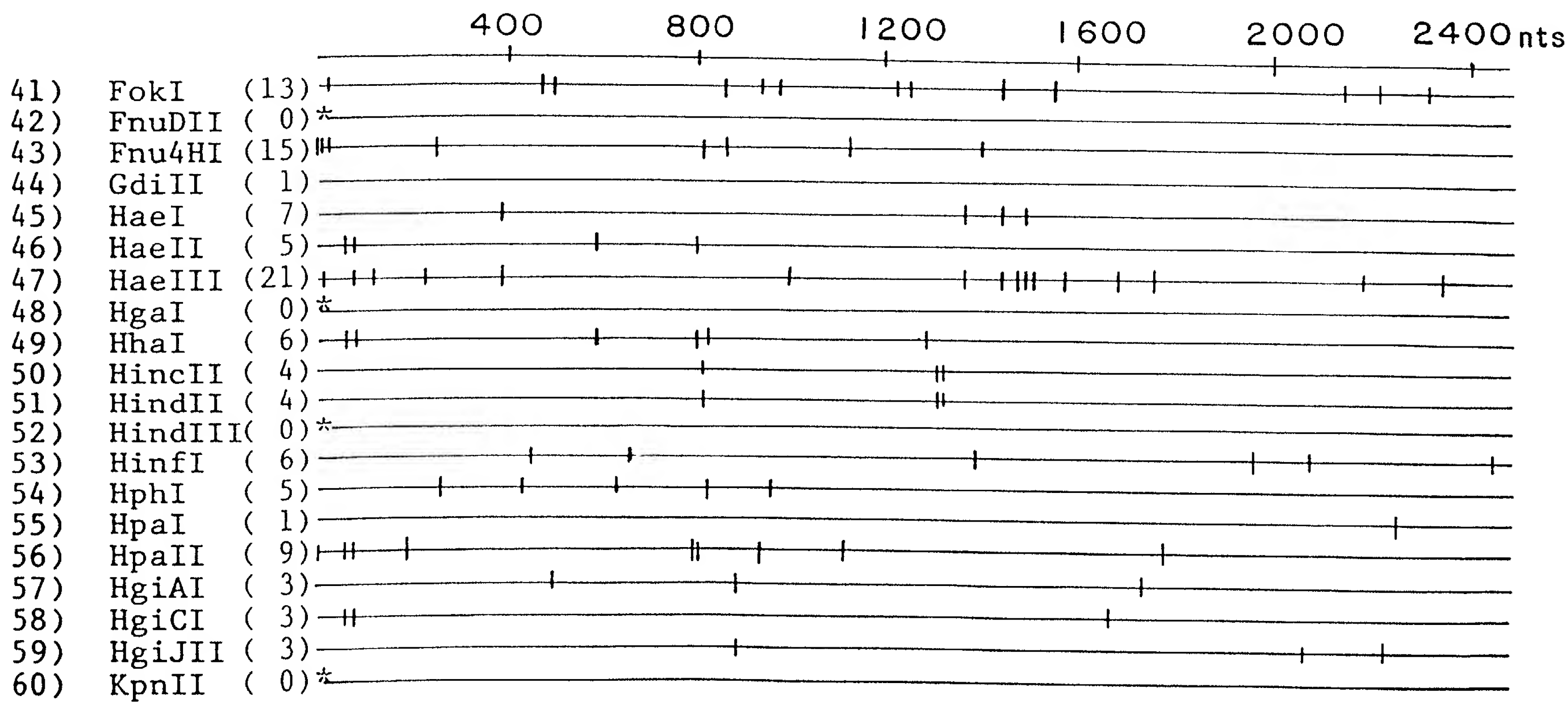

400
800
1200
1600
2000
2400nts
41) FokI (13)
42) FnuDII (0)*
43) Fnu4HI (15)
44) GdiII (1)
45) HaeI (7)
46) HaeII (5)
47) HaeIII (21)
48) HgaI (0)*
49) HhaI (6)
50) HincII (4)
51) HindII (4)
52) HindIII(0)*
53) HinfI (6)
54) HphI (5)
55) HpaI (1)
56) HpaII (9)
57) HgiAI (3)
58) HgiCI (3)
59) HgiJII (3)
60) KpnII (0)*

FIG. 6C

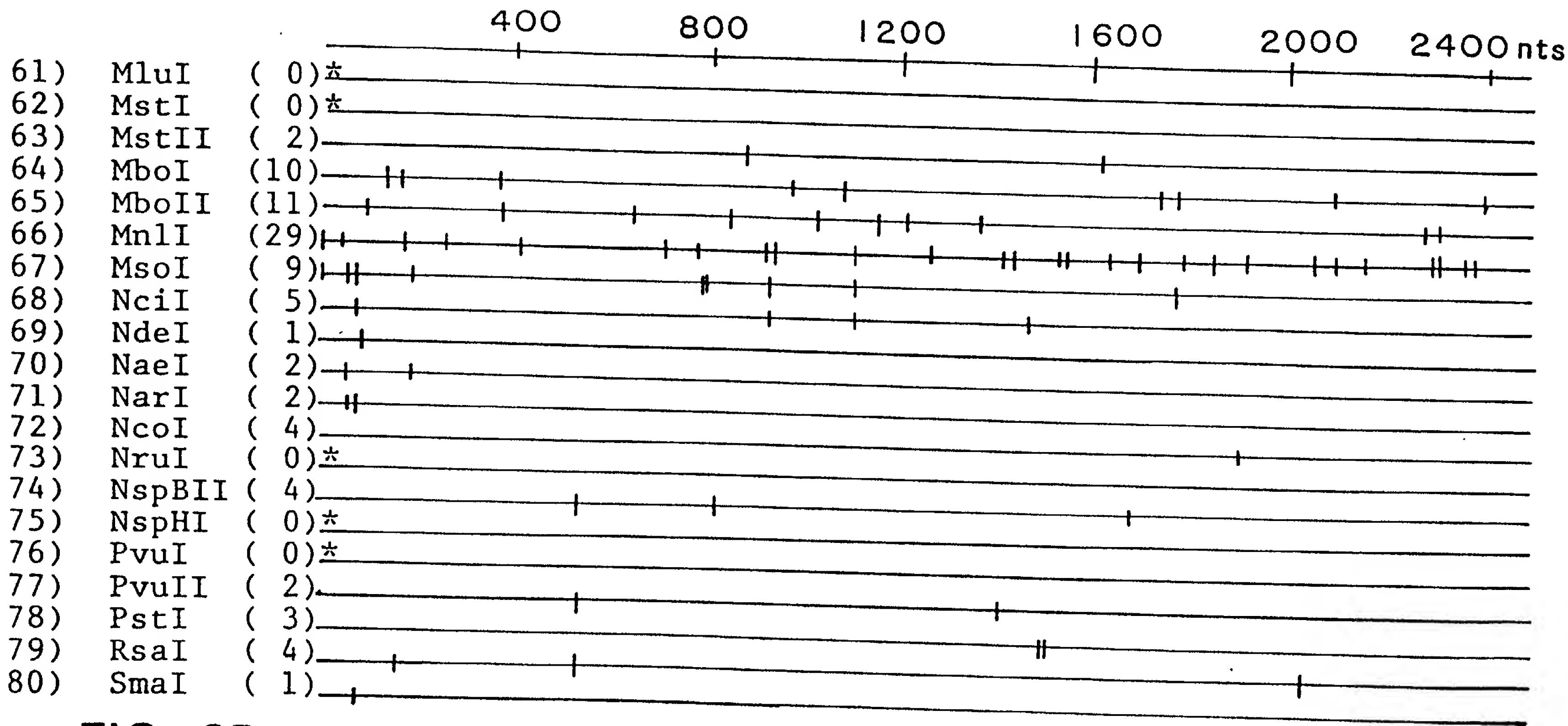

400
800
1200
1600
2000
2400 nts
61) MluI (0)*
62) MstI (0)*
63) MstII (2)
64) MboI (10)
65) MboII (11)
66) MnlI (29)
67) MsoI (9)
68) NciI (5)
69) NdeI (1)
70) NaeI (2)
71) NarI (2)
72) NcoI (4)
73) NruI (0)*
74) NspBII (4)
75) NspHI (0)*
76) PvuI (0)*
77) PvuII (2)
78) PstI (3)
79) RsaI (4)
80) SmaI (1)

FIG. 6D

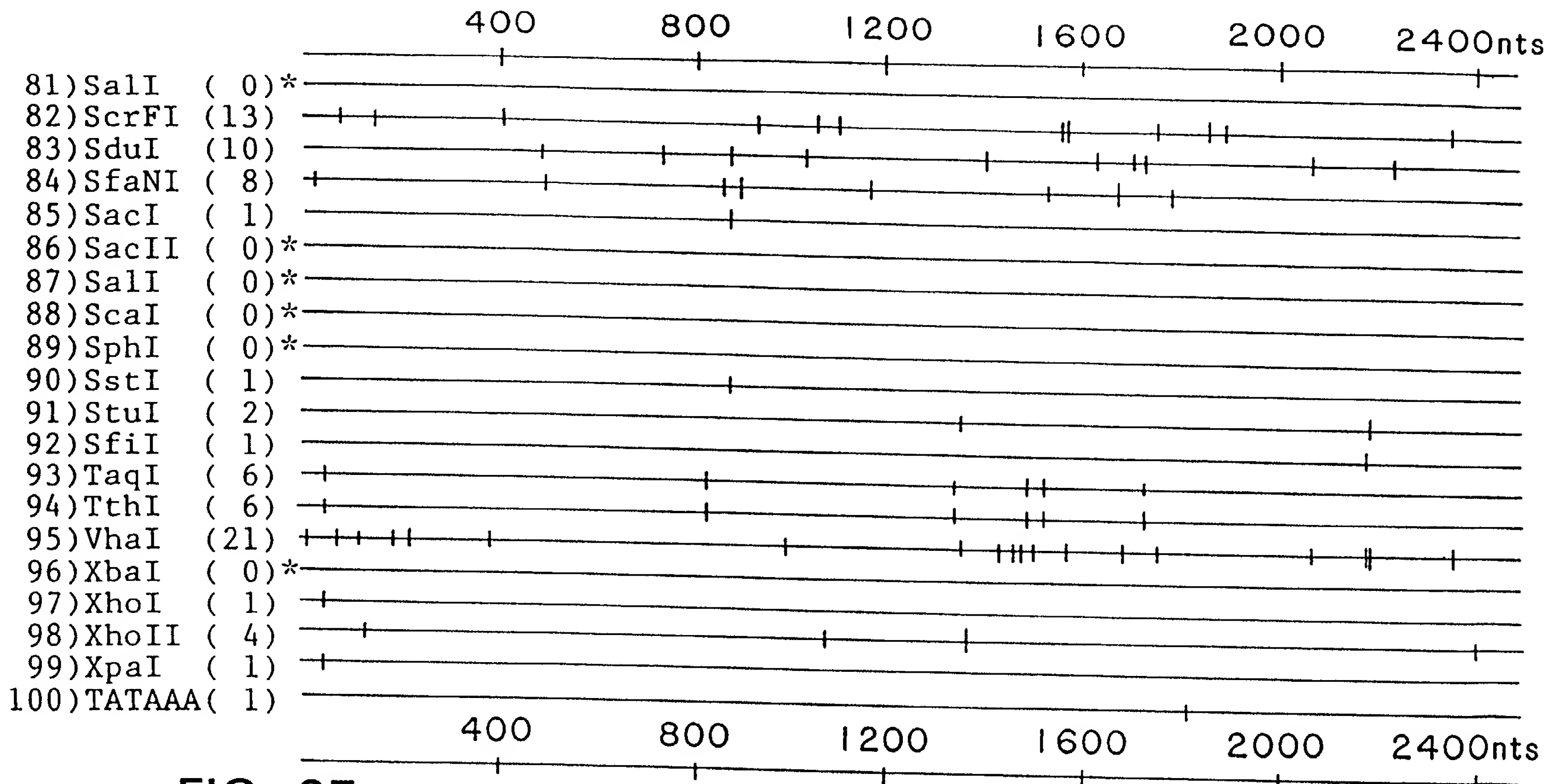

400
800
1200
1600
2000
2400nts
81)SalI (0)*
82)ScrFI (13)
83)SduI (10)
84)SfaNI (8)
85)SacI (1)
86)SacII (0)*
87)SalI (0)*
88)ScaI (0)*
89)SphI (0)*
90)SstI (1)
91)StuI (2)
92)SfiI (1)
93)TaqI (6)
94)TthI (6)
95)VhaI (21)
96)XbaI (0)*
97)XhoI (1)
98)XhoII (4)
99)XpaI (1)
100)TATAAA(1)
400
800
1200
1600
2000
2400nts

FIG. 6E

FIG. 7A

```
                                    27                                54
3'GTC GGG TGG GCT CTC CTG GGC CAT GTC GGG GTA GGG TGG GTC GGT GGT GGT CGA5'
5'CAG CCC ACC CGA GAG GAC CCG GTA CAG CCC CAT CCC ACC CAG CCA CCA CCA GCT3'
  Gln Pro Thr Arg Glu Asp Pro Val Gln Pro His Pro Thr Gln Pro Pro Pro Ala
   Ser Pro Pro Glu Arg Thr Arg Tyr Ser Pro Ile Pro Pro Ser His His Gln Leu
    Ala His Pro Arg Gly Pro Gly Thr Ala Pro Ser His Pro Ala Thr Thr Ser

                                    81                               108
  CTG AGA GGG GCT GGG CAG GGT GGT ACC AGA GGT GTC GTG AGG GCT GTC GGG GCG
  GAC TCT CCC CGA CCC GTC CCA CCA TGG TCT CCA CAG CAC TCC CGA CAG CCC CGC
  Asp Ser Pro Arg Pro Val Pro Pro Trp Ser Pro Gln His Ser Arg Gln Pro Arg
   Thr Leu Pro Asp Pro Ser His His Gly Leu His Ser Thr Pro Asp Ser Pro Ala
    Leu Ser Pro Thr Arg Pro Thr MET Val Ser Thr Ala Leu Pro Thr Ala Pro Pro

                                   135                               162
  GTT TGG TCT CTT CTT ACC CGT ACG GTT TTC CTG GTG GGG TTC CTA ACG GTT CTA
  CAA ACC AGA GAA GAA TGG GCA TGC CAA AAG GAC CAC CCC AAG GAT TGC CAA GAT
  Gln Thr Arg Glu Glu Trp Ala Cys Gln Lys Asp His Pro Lys Asp Cys Gln Asp
   Lys Pro Glu Lys Asn Gly His Ala Lys Arg Thr Thr Pro Arg Ile Ala Lys Ile
    Asn Gln Arg Arg MET Gly MET Pro Lys Gly Pro Pro Gln Gly Leu Pro Arg Ser

                                   189                               216
  GAA ACT CTA GGT CTG GTA CGG GTT ACC GTT TTG GGC CTG GAG GGA GTT CTG GTA
  CTT TGA GAT CCA GAC CAT GCC CAA TGG CAA AAC CCG GAC CTC CCT CAA GAC CAT
  Leu  .  Asp Pro Asp His Ala Gln Trp Gln Asn Pro Asp Leu Pro Gln Asp His
   Phe Glu Ile Gln Thr MET Pro Asn Gly Lys Thr Arg Thr Ser Leu Lys Thr MET
```

FIG. 7B

```
                                   243                                                   270
CTC GGC ATC CTT C6A G55 GGT CGT CTT CCT CTT CTT TCG GTG AGT CTA CGA GCG
GAG CCG TAG GAA G3T C44 CCA GCA GAA GGA GAA GAA AGC CAC TCA GAT GCT CGC
Glu Pro  .  Glu C    TT Pro Ala Glu Gly Glu Glu Ser His Ser Asp Ala Arg
 Ser Arg Arg Lys Leu Phe Gln Gln Lys Glu Lys Lys Ala Thr Gln MET Leu Ala
  Ala Val Gly     Ser     Ser Arg Arg Arg Arg Lys Pro Leu Arg Cys Ser Pro

                                   297                                                   324
GTA 5CA AGA GCC GCA CAA GTA GTA GAC GAC CGA CGG GAA GAA GTA GTG TGT GTA
CAT 4GT TCT CGG CGT GTT CAT CAT CTG CTG GCT GCC CTT CTT CAT CAC ACA CAT
His T   Ser Arg Arg Val His His Leu Leu Ala Ala Leu Leu His His Thr His
 ILE Val Leu Gly Val Phe Ile Ile Cys Trp Leu Pro Phe Phe Ile Thr His Ile
  le  Phe Ser Ala Cys Ser Ser Ser Ala Gly Cys Pro Ser Ser Ser His Thr Ser

                                   351                                                   378
GGA CTT GTA TGT GAC ACT GAC GTT GTA GGG CGG ACA GGA CAT GTC GCG GAA GTG
CCT GAA CAT ACA CTG TGA CTG CAA CAT CCC GCC TGT CCT GTA CAG CGC CTT CAC
Pro Glu His Thr Leu  .  Leu Gln His Pro Ala Cys Pro Val Gln Arg Leu His
 Leu Asn Ile His Cys Asp Cys Asn Ile Pro Pro Val Leu Tyr Ser Ala Phe Thr
  .  Thr Tyr Thr Val Thr Ala Thr Ser Arg Leu Ser Cys Thr Ala Pro Ser Arg

                                   405                                                   432
CAC CGA CCC GAT ACA GTT GTC GCG GCA CTT GGG GTA GTA GAT GTG GTG GAA GTT
GTG GCT GGG CTA TGT CAA CAG CGC CGT GAA CCC CAT CAT CTA CAC CAC CTT CAA
Val Ala Gly Leu Cys Gln Gln Arg Arg Glu Pro His His Leu His His Leu Gln
 Trp Leu Gly Tyr Val Asn Ser Ala Val Asn Pro Ile Ile Tyr Thr Thr Phe Asn
  Gly Trp Ala MET Ser Thr Ala Pro  .  Thr Pro Ser Ser Thr Pro Pro Ser Thr
```

```
                                    459                                   486
GTA ACT CAA GGC GTT CCG GAA GGA CTT CTA GGA GGT GAC GAC TGA GAC GAC GGA
CAT TGA GTT CCG CAA GGC CTT CCT GAA GAT CCT CCA CTG CTG ACT CTG CTG CCT
His  .  Val Pro Gln Gly Leu Pro Glu Asp Pro Pro Leu Leu Thr Leu Leu Pro
 Ile Glu Phe Arg Lys Ala Phe Leu Lys Ile Leu His Cys STOPLeu Cys Cys Leu
  Leu Ser Ser Ala Arg Pro Ser  .  Arg Ser Ser Thr Ala Asp Ser Ala Ala Cys

                                    513                                   540
CGG CGT GTC GTC GGA CGA AGG GTG GAG GGA CGG GTC ACG GCC GGT CGG AGT GGG
GCC GCA CAG CAG CCT GCT TCC CAC CTC CCT GCC CAG TGC CGG CCA GCC TCA CCC
Ala Ala Gln Gln Pro Ala Ser His Leu Pro Ala Gln Cys Arg Pro Ala Ser Pro
 Pro His Ser Ser Leu Leu Pro Thr Ser Leu Pro Ser Ala Gly Gln Pro His Pro
  Arg Thr Ala Ala Cys Phe Pro Pro Pro Cys Pro Val Pro Ala Ser Leu Thr Leu

                                    567                                   594
AAC GCT TGG CAC TCG TCC TTC CGG ACC CAC CTA GCC GGA GGA GAA GAT CGG GGC
TTG CGA ACC GTG AGC AGG AAG GCC TGG GTG GAT CGG CCT CCT CTT CTA GCC CCG
Leu Arg Thr Val Ser Arg Lys Ala Trp Val Asp Arg Pro Pro Leu Leu Ala Pro
 Cys Glu Pro  .  Ala Gly Arg Pro Gly Trp Ile Gly Leu Leu Phe  .  Pro Arg
  Ala Asn Arg Glu Gln Glu Gly Leu Gly Gly Ser Ala Ser Ser Ser Ser Pro Gly
```

FIG. 7C

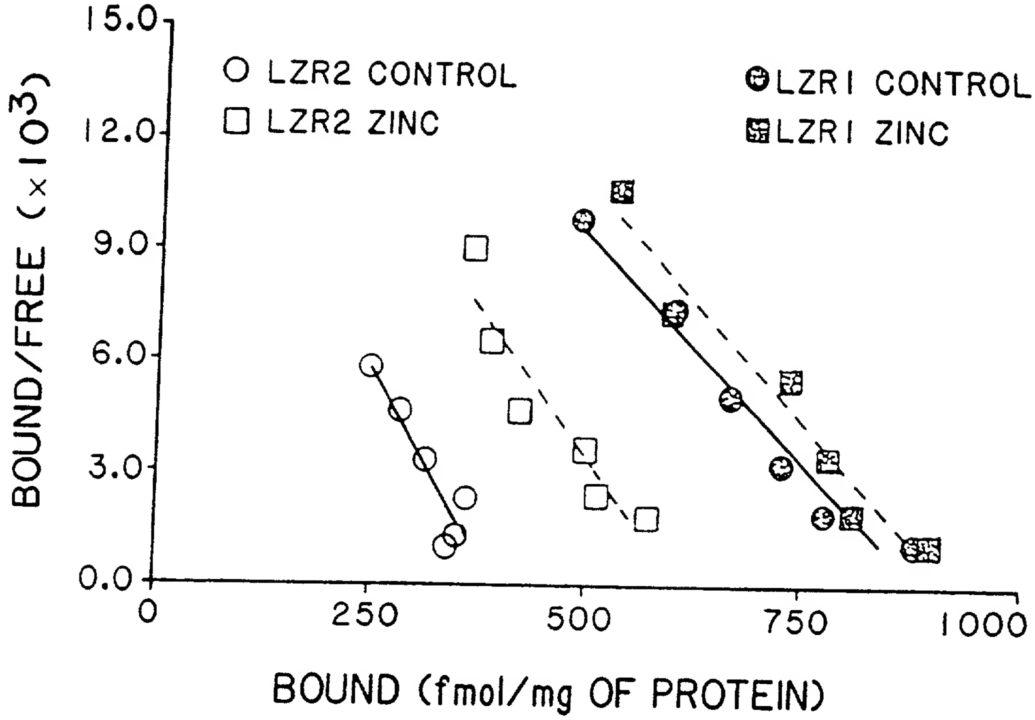

15.0
12.0
9.0
6.0
3.0
0.0
BOUND/FREE (×10³)
LZR2 CONTROL
LZR2 ZINC
LZR1 CONTROL
LZR1 ZINC
0
250
500
750
1000
BOUND (fmol/mg OF PROTEIN)

FIG. 8

FIG. 11

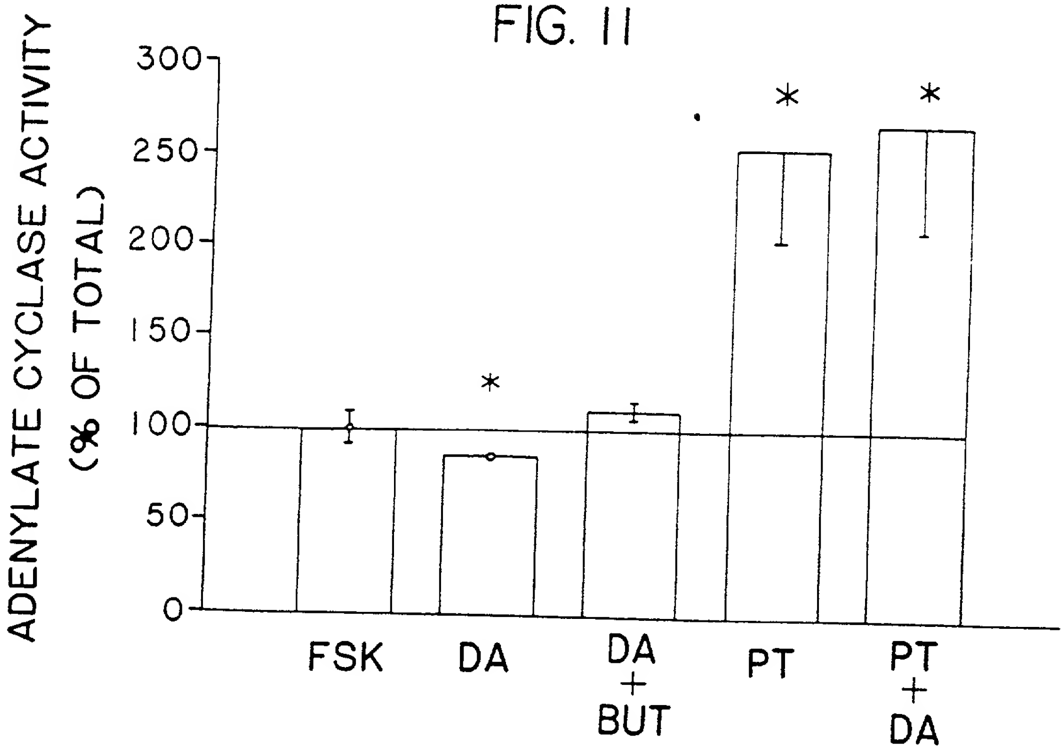

ADENYLATE CYCLASE ACTIVITY
(% OF TOTAL)
300
250
200
150
100
50
0
*
*
*
FSK
DA
DA + BUT
PT
PT + DA

FIG. 9A

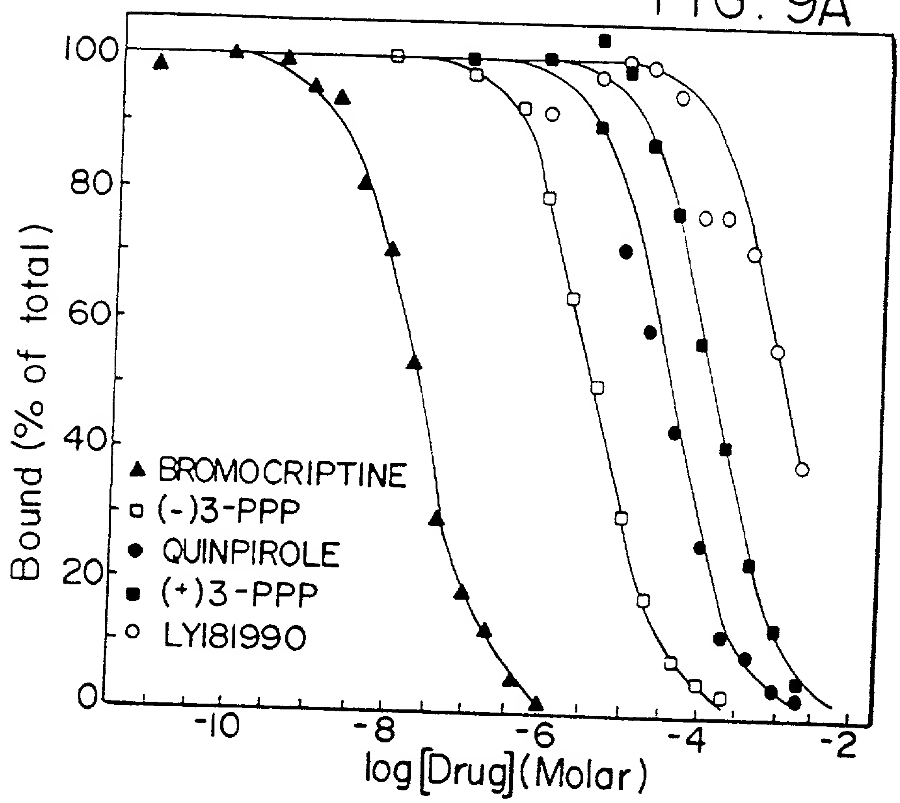
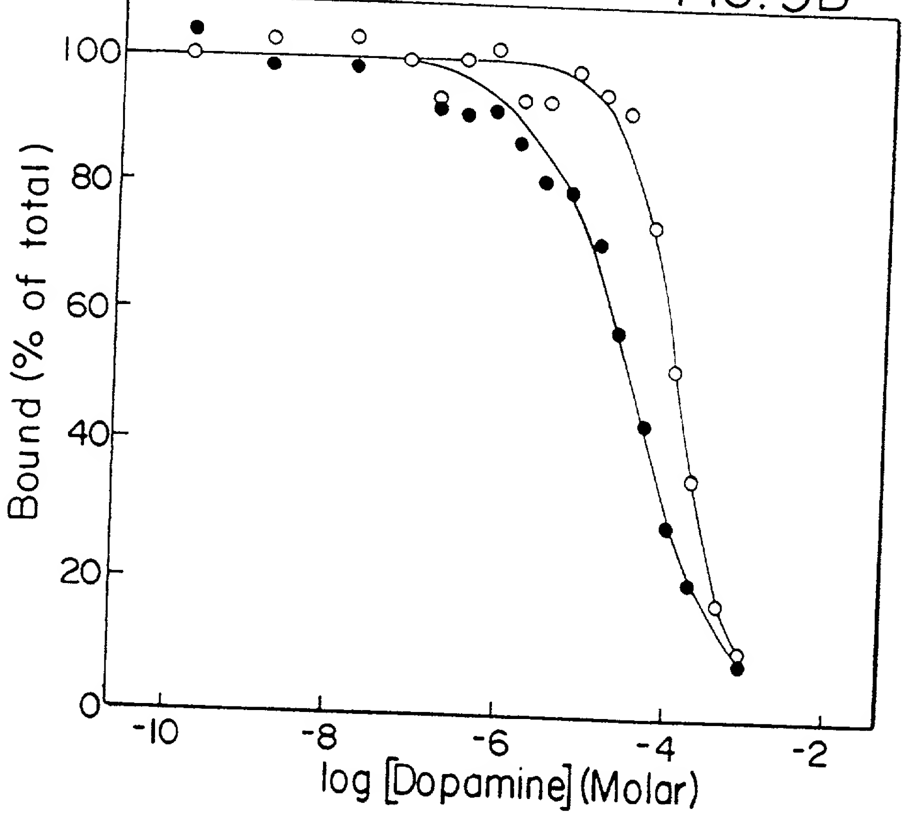

Bound (% of total)
100
80
60
40
20
0
BROMOCRIPTINE
(-)3-PPP
QUINPIROLE
(+)3-PPP
LY181990
-10
-8
-6
-4
-2
log [Drug] (Molar)

FIG. 9B


Bound (% of total)
100
80
60
40
20
0
-10
-8
-6
-4
-2
log [Dopamine] (Molar)

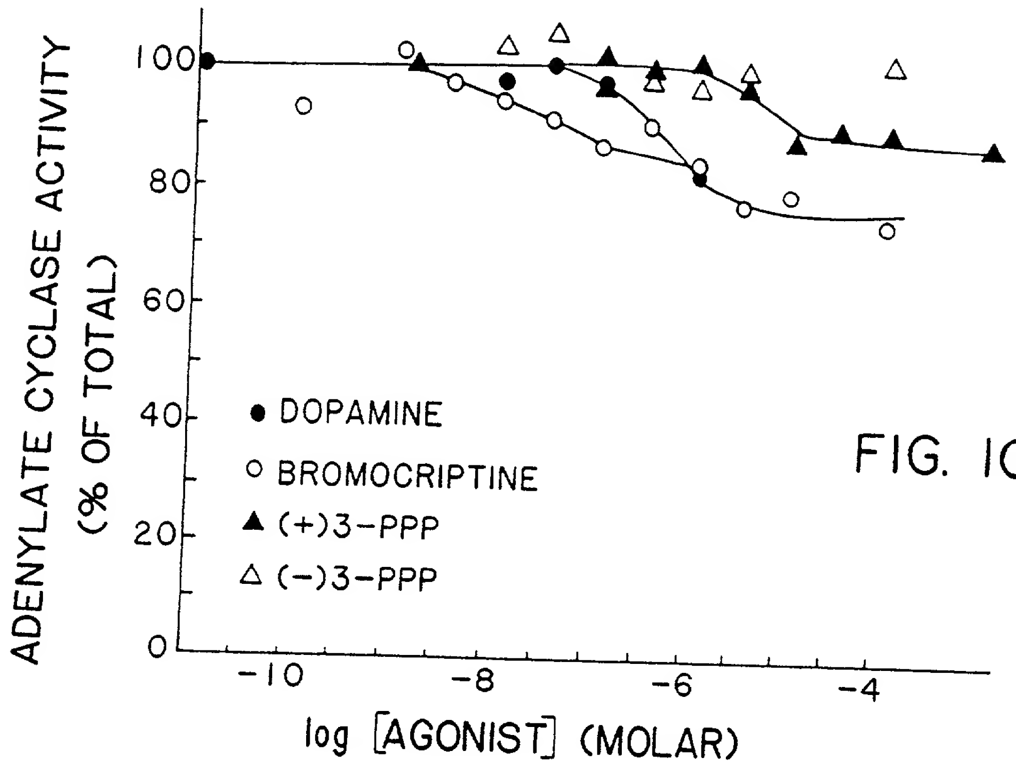


FIG. 10A

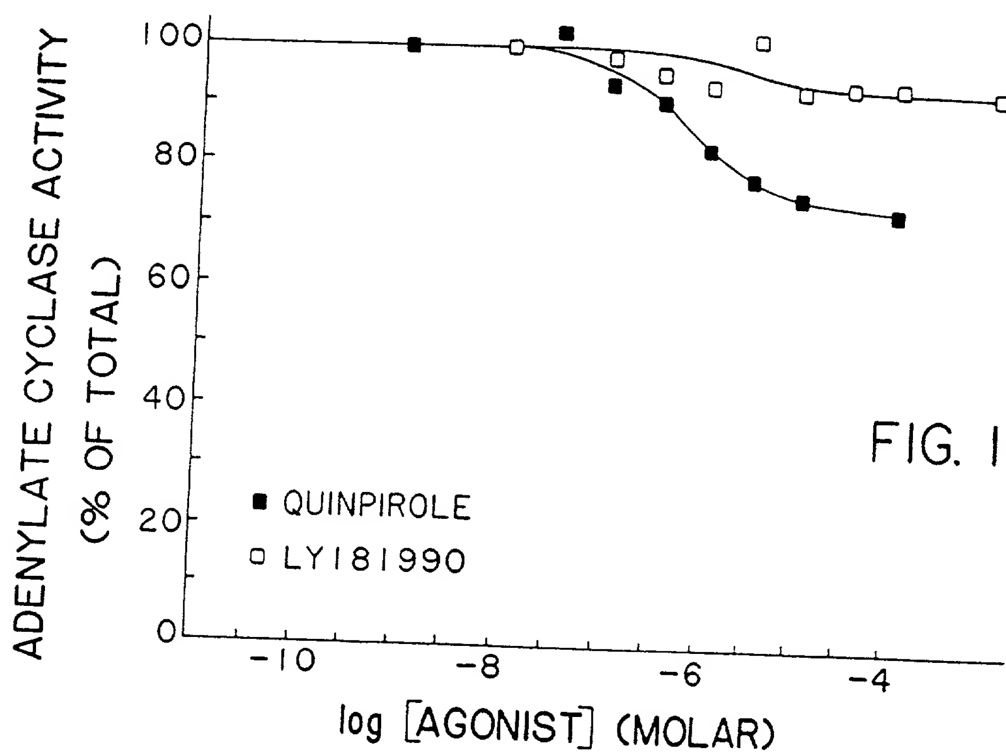


FIG. 10B

FIG. 12A

	CONTROL			+P.T.		
	BASAL	FSK	FSK+DA	BASAL	FSK	FSK+DA
$\overline{X}$	2.1	22.6	14.3	1.7	26.7	23.1
S.E.	0.2	2.2	2.1	0.4	2.0	0.5
INH	—	—	41%	—	—	14%

FIG. 12B

	CONTROL				+P.T.			
	BASAL	VIP	DA	VIP+DA	BASAL	VIP	DA	VIP+DA
$\overline{X}$	0.60	2.41	0.32	0.84	0.61	2.68	0.55	2.56
S.E.	0.02	0.31	0.02	0.13	0.09	0.08	0.03	0.25
INH	—	—	53%	71%	—	—	10%	3%

FIG. 12C

	CONTROL				+P.T.			
	BASAL	VIP	DA	VIP+DA	BASAL	VIP	DA	VIP+DA
$\overline{X}$	0.78	5.1	0.25	0.76	0.64	5.29	0.66	4.76
S.E.	0.04	0.4	0.03	0.01	0.01	0.44	0.03	0.16
INH	—	—	68%	88%	—	—	0%	12%

FIG. 13B-1

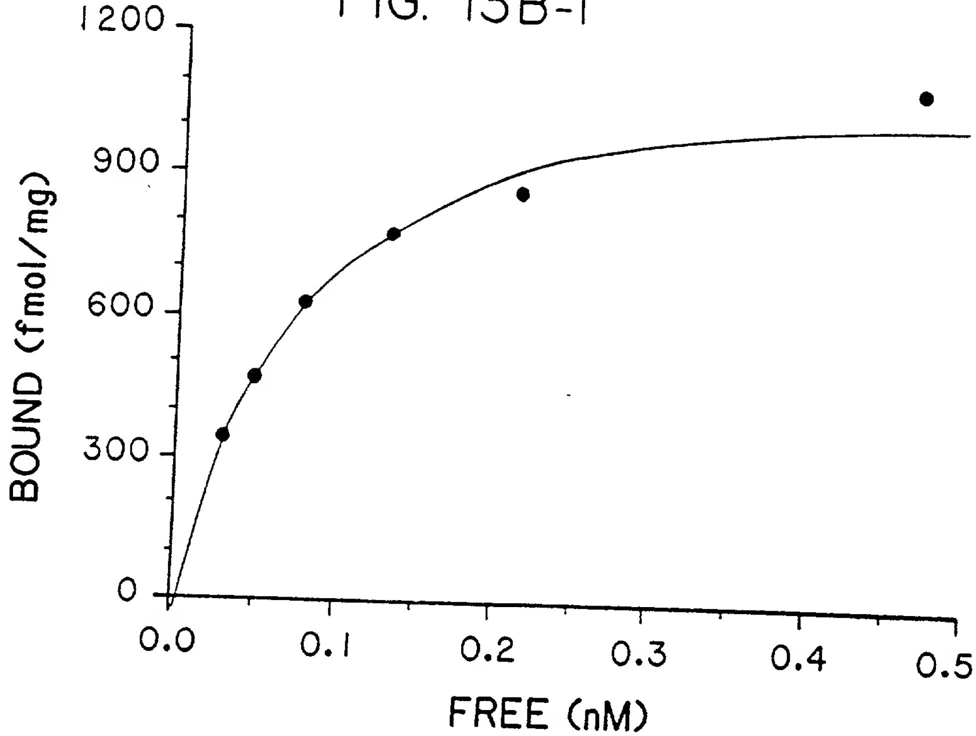


FIG. 13B-2

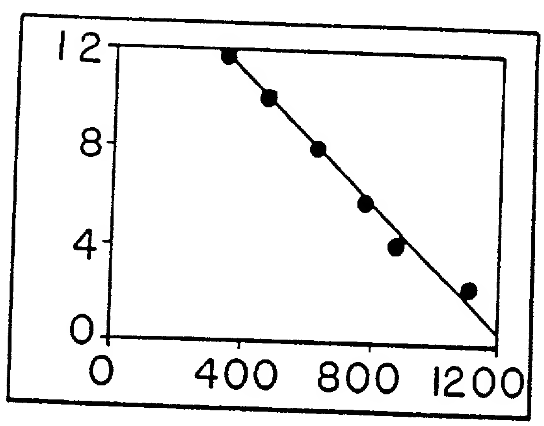
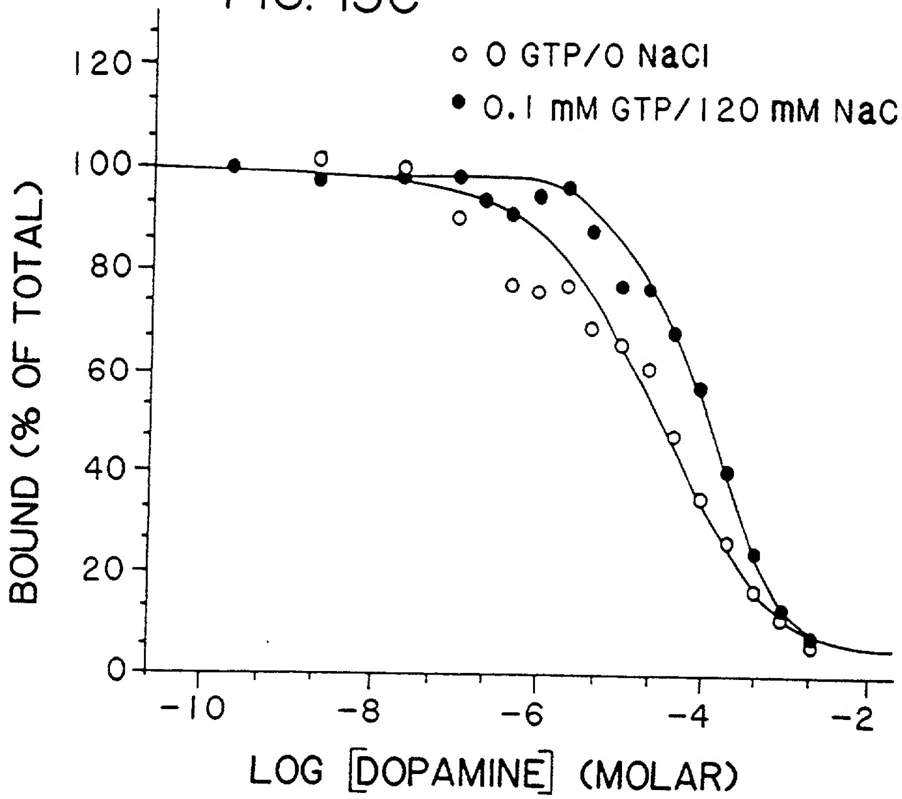


FIG. 13C



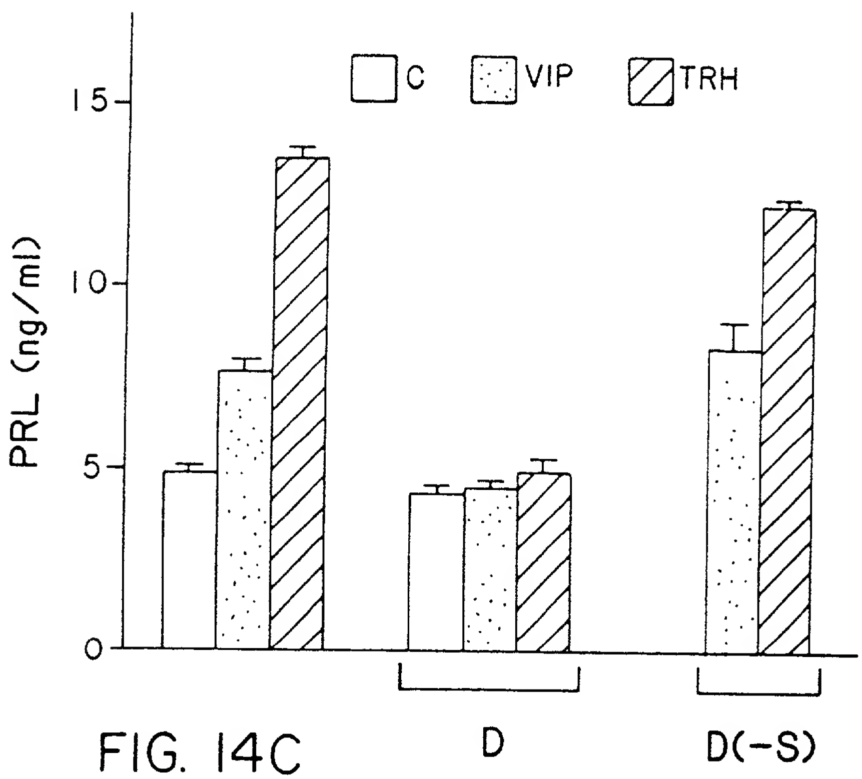


FIG. 14C

FIG.14A

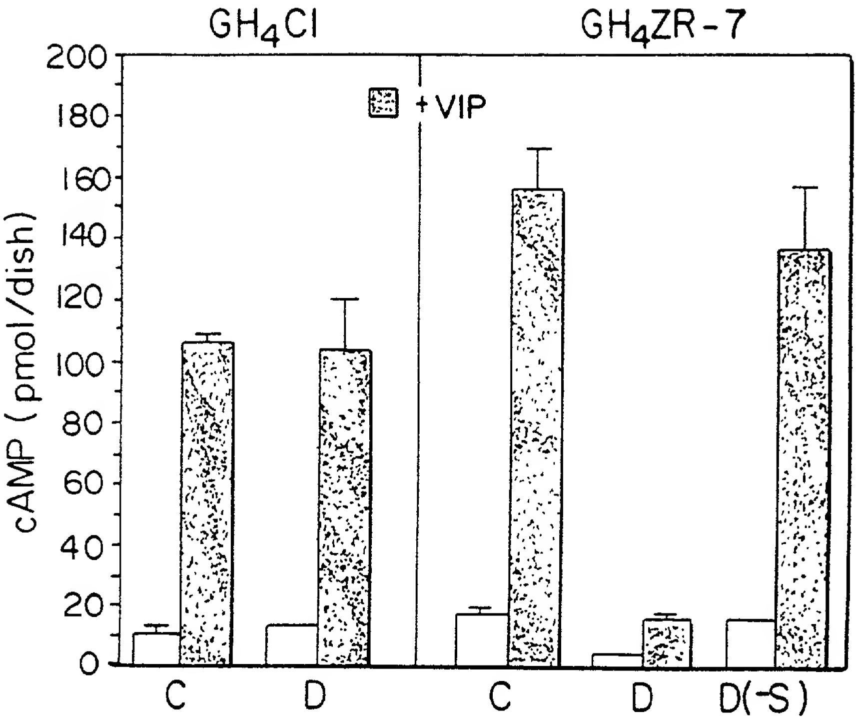
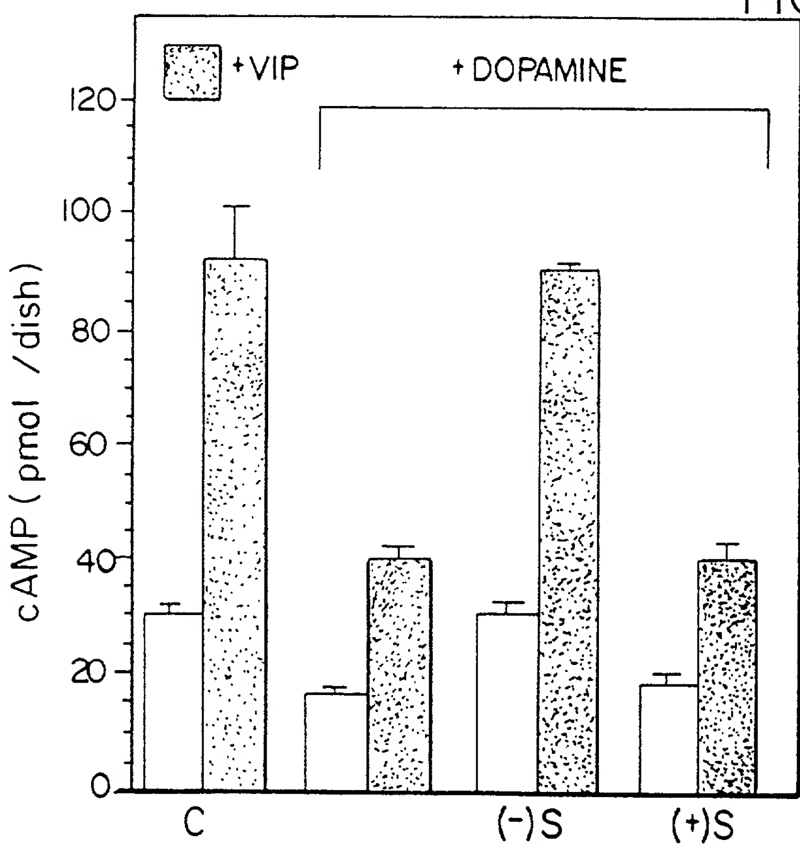


FIG.14B



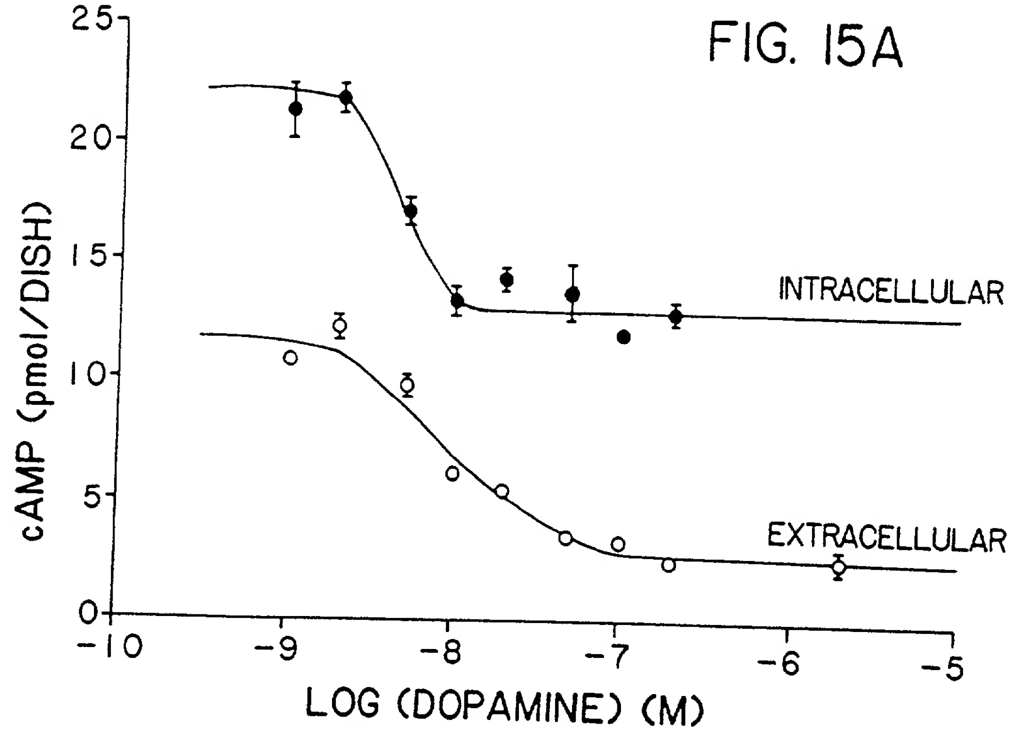


FIG. 15A

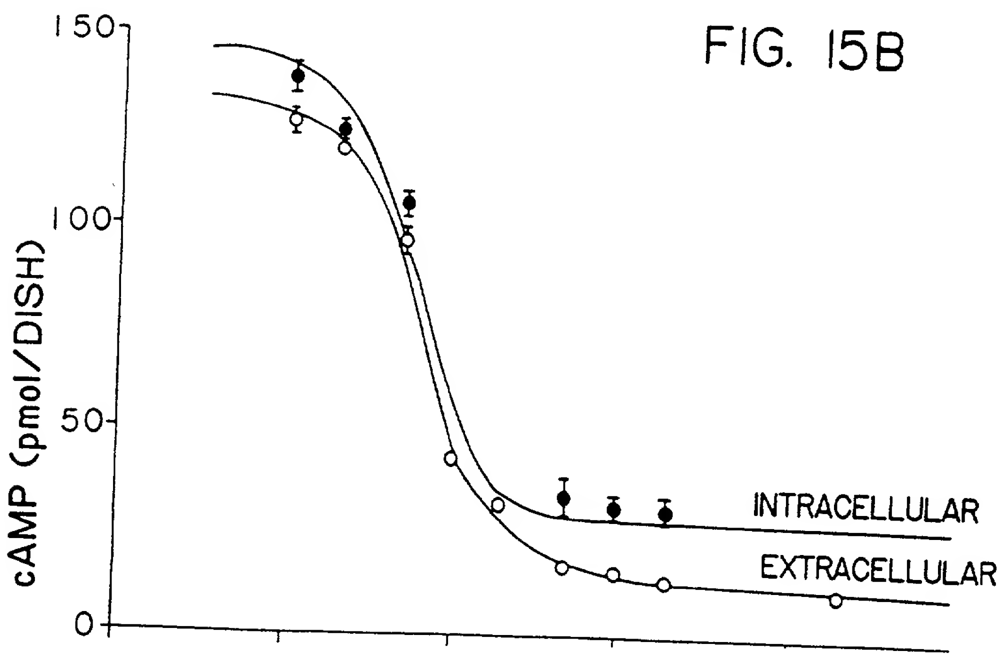
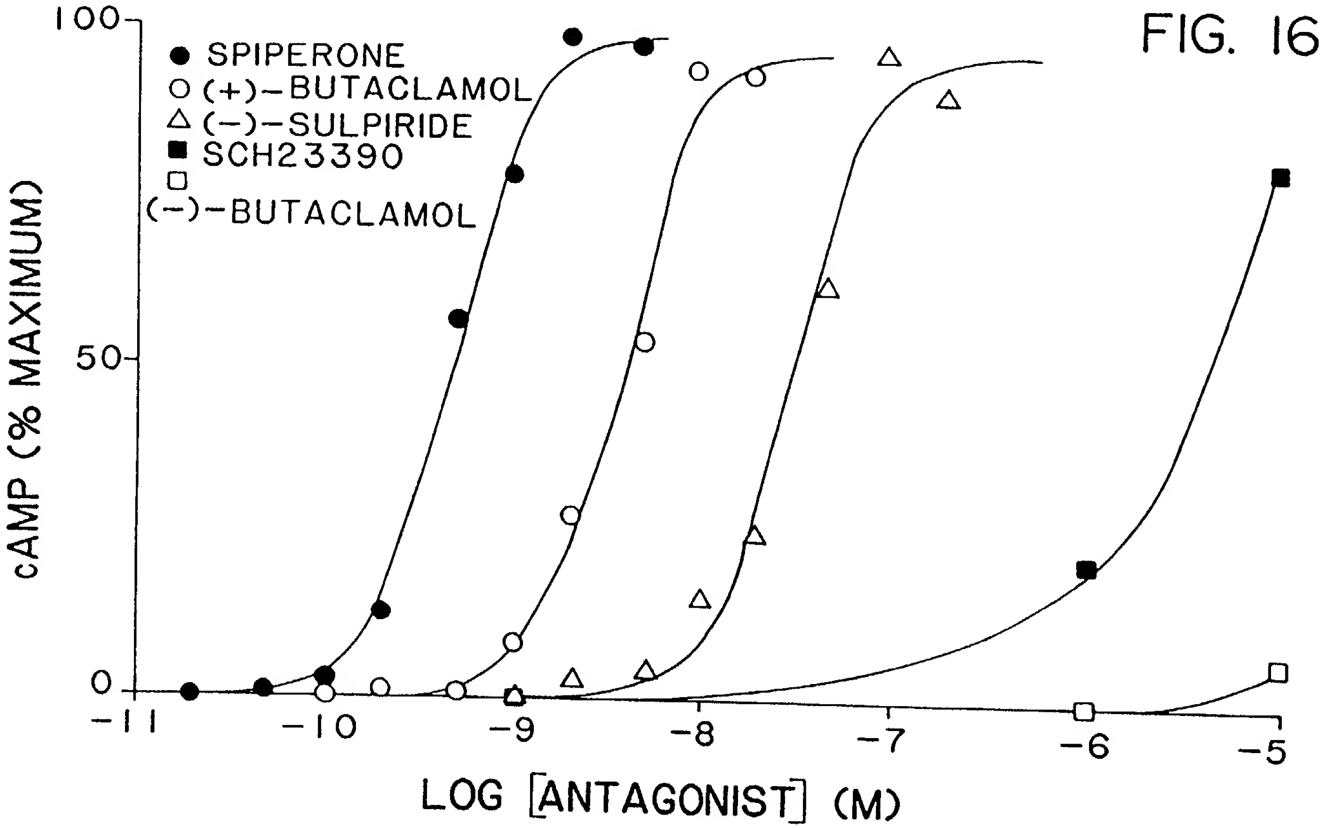


FIG. 15B

FIG. 16



SPIPERONE
(+)-BUTACLAMOL
(−)-SULPIRIDE
SCH23390
(−)-BUTACLAMOL
cAMP (% MAXIMUM)
100
50
0
−11
−10
−9
−8
−7
−6
−5
LOG [ANTAGONIST] (M)

FIG.17A

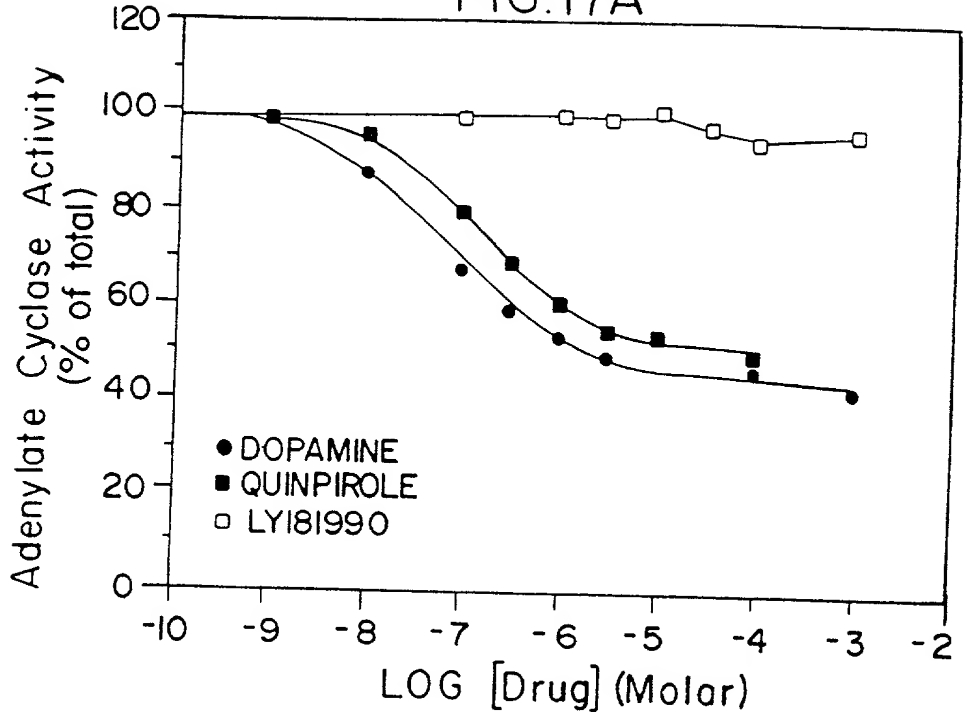
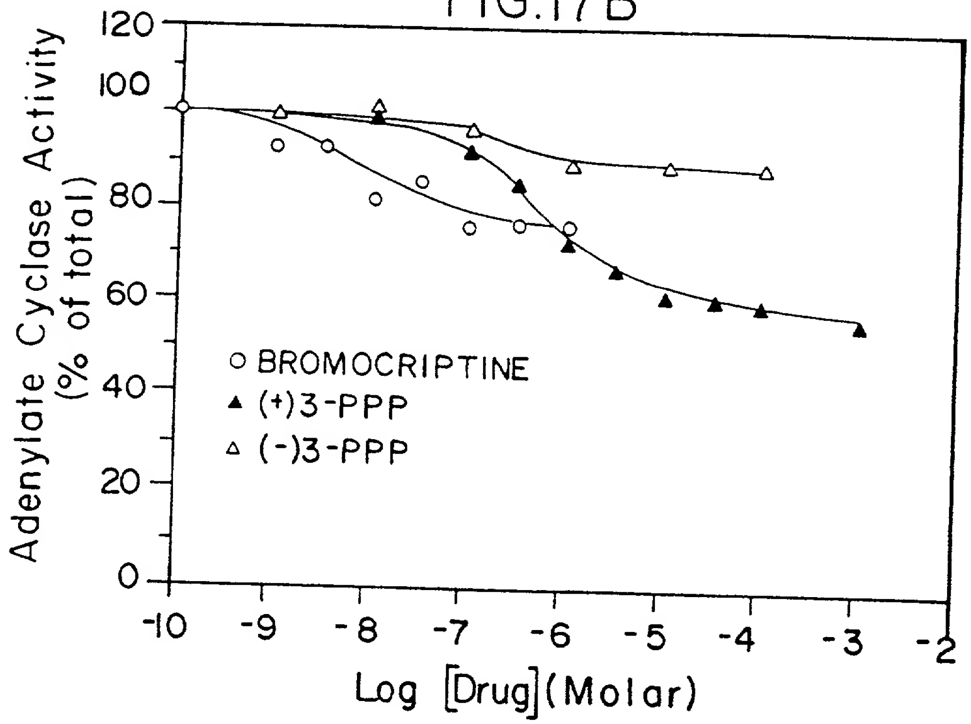


FIG.17B



```
-33 AGAGCCTGGCCACCCAGTGGCTCCACCGCCCTG

                                             10                                     20
METAspProLeuAsnLeuSerTrpTyrAspAspAspLeuGluArgGlnAsnTrpSerArg
ATGGATCCACTGAATCTGTCCTGGTATGATGATGATCTGGAGAGGCAGAACTGGAGCCGG
|||||||||||||| ||||||||||| ||||| ||||||||||||||||||||||||
ATGGATCCACTGAACCTGTCCTGGTACGATGACGATCTGGAGAGGCAGAACTGGAGCCGG

                                             30                                     40
ProPheAsnGlySerAspGlyLysAlaAspArgProHisTyrAsnTyrTyrAlaThrLeu
CCCTTCAACGGGTCAGACGGGAAGGCGGACAGACCCCACTACAACTACTATGCCACACTG
|||||||| |||||||| |||||||| ||||| ||||||||||||||||||||||  |||
CCCTTCAATGGGTCAGAAGGGAAGGCAGACAGGCCCCACTACAACTACTATGCCATGCTG    120
                  Glu                                     MET
```

FIG. 18A

```
                                       50                                60
LeuThrLeuLeuIleAlaValIleValPheGlyAsnValLeuValCysMETAlaValSer
CTCACCCTGCTCATCGCTGTCATCGTCTTCGGCAACGTGCTGGTGTGCATGGCTGTGTCC
CTCACCCTCCTCATCTTTATCATCGTCTTTGGCAATGTGCTGGTGTGCATGGCTGTATCC
               PheIle

                                       70                                80
ArgGluLysAlaLeuGlnThrThrThrAsnTyrLeuIleValSerLeuAlaValAlaAsp
CGCGAGAAGGCGCTGCAGACCACCACCAACTACCTGATCGTCAGCCTCGCAGTGGCCGAC
CGAGAGAAGGCTTTGCAGACCACCACCAACTACTTGATAGTCAGCCTTGCTGTGGCTGAT    240

                                       90                                100
LeuLeuValAlaThrLeuValMETProTrpValValTyrLeuGluValValGlyGluTrp
CTCCTCGTCGCCACACTGGTCATGCCCTGGGTTGTCTACCTGGAGGTGGTAGGTGAGTGG
CTTCTGGTGGCCACACTGGTAATGCCGTGGGTTGTCTACCTGGAGGTGGTGGGTGAGTGG
```

FIG. 18B

```
                                  110                       111      120
LysPheSerArgIleHisCysAspIlePheValThrLeuAspValMETMETCysThrAla
AAATTCAGCAGGATTCACTGTGACATCTTCGTCACTCTGGACGTCATGATGTGCACGGCG
||||||||||||||||||||||||||||| ||||||||||| |||||||||||||| ||      360
AAATTCAGCAGGATTCACTGTGACATCTTTGTCACTCTGGATGTCATGATGTGCACAGCA

                          130                          140
SerIleLeuAsnLeuCysAlaIleSerIleAspArgTyrThrAlaValAlaMETProMET
                                   ▼
AGCATCCTGAACTTGTGTGCCATCAGCATCGACAGGTACACAGCTGTGGCCATGCCCATG
|||||||||||| |||||||||||||||| |||||||||||||||||||| |||||||||
AGCATCCTGAACCTGTGTGCCATCAGCATTGACAGGTACACAGCTGTGGCAATGCCCATG

                          150                          160
LeuTyrAsnThrArgTyrSerSerLysArgArgValThrValMETIleSerIleValTrp
CTGTACAATACGCGCTACAGCTCCAAGCGCCGGGTCACCGTCATGATCTCCATCGTCTGG
||||| || || |||||||||||||||||||| || || ||||||||  |||| ||||||     480
CTGTATAACACACGCTACAGCTCCAAGCGCCGAGTTACTGTCATGATTGCCATTGTCTGG
                                                    Ala
```

FIG. 18C

```
IV
ValLeuSerPheThrIleSerCysProLeuLeuPheGlyLeuAsnAsnAlaAspGlnAsn
                          170                           180
GTCCTGTCCTTCACCATCTCCTGCCCACTCCTCTTCGGACTCAATAACGCAGACCAGAAC
GTCCTGTCCTTCACCATCTCCTGCCCACTGCTCTTCGGACTCAACAATACAGACCAGAAT
                                                 Thr

GluCysIleIleAlaAsnProAlaPheValValTyrSerSerIleValSerPheTyrVal
                          190           V               200
GAGTGCATCATTGCCAACCCGGCCTTCGTGGTCTACTCCTCCATCGTCTCCTTCTACGTG
GAGTGTATCATTGCCAACCCTGCCTTTGTGGTCTACTCCTCCATTGTCTCATTCTACGTG   600

ProPheIleValThrLeuLeuValTyrIleLysIleTyrIleValLeuArgArgArgArg
                          210                           220
CCCTTCATTGTCACCCTGCTGGTCTACATCAAGATCTACATTGTCCTCCGCAGACGCCGC
CCCTTCATCGTCACTCTGCTGGTCTATATCAAAATCTACATCGTCCTCCGGAAGCGCCGG
                                                     Lys
```

FIG. 18D

```
                          230                     240
LysArgValAsnThrLysArgSerSerArgAlaPheArgAlaHisLeuArgAlaProLeu
         .         .         .         .         .         .
AAGCGAGTCAACACCAAACGCAGCAGCCGAGCTTTCAGGGCCCACCTGAGGGCTCCACTA
||||| ||||||||||| |||||||| ||||||||||| || |||||| | | |||||     720
AAGCGGGTCAACACCAAGCGCAGCAGTCGAGCTTTCAGAGCCAACCTGAAGACACCACTC
                                          Asn   LysThr

    *                     250                              *
LysGlyAsnCysThrHisProGluAspMETLysLeuCysThrValIleMETLysSerAsn
  ▼      .         .         .         .         .         .
AAGGGCAACTGTACTCACCCCGAGGACATGAAACTCTGCACCGTTATCATGAAGTCTAAT
!!!
AAG.........................................................

                          270                     280
GlySerPheProValAsnArgArgArgValGluAlaAlaArgArgAlaGlnGluLeuGlu
         .         .         ▼         .         .         .
GGGAGTTTCCCAGTGAACAGGCGGAGAGTGGAGGCTGCCCGGCGAGCCCAGGAGCTGGAG
                              || |||||||| ||||| |||||||||||
..............................GATGCTGCCCGCCGAGCTCAGGAGCTGGAA   840
                              Asp
```

FIG. 18E

```
                             290                         300
METGluMETLeuSerSerThrSerProProGluArgThrArgTyrSerProIleProPro
ATGGAGATGCTCTCCAGCACCAGCCCACCCGAGAGGACCCGGTACAGCCCCATCCCACCC
||||||||||| || ||||||||||| || |||||||||||||| ||||||||||| |||
ATGGAGATGCTGTCAAGCACCAGCCCCCCAGAGAGGACCCGGTATAGCCCCATCCCTCCC

                             310                         320
SerHisHisGlnLeuThrLeuProAspProSerHisHisGlyLeuHisSerThrProAsp
AGCCACCACCAGCTGACTCTCCCCGACCCGTCCCACCATGGTCTCCACAGCACTCCCGAC
|| ||||||||||| |||||||| || || |||||||| || || || ||||  || |||   960
AGTCACCACCAGCTCACTCTCCCTGATCCATCCCACCACGGCCTACATAGCAACCCTGAC
                                                Asn

                             330                         339
SerProAlaLysProGluLysAsnGlyHisAlaLys   AspHisProLysIleAlaLys
AGCCCCGCCAAACCAGAGAAGAATGGGCATGCCAAA...GACCACCCCAAGATTGCCAAG
|| || ||||||||||||||||||||||| |||||    | | | |||| ||||||||||
AGTCCTGCCAAACCAGAGAAGAATGGGCACGCCAAGATTGTCAATCCCAGGATTGCCAAG
                                    IleValAsn   Arg
```

FIG. 18F

```
                         349                                     359
IlePheGluIleGlnThrMETProAsnGlyLysThrArgThrSerLeuLysThrMETSer
ATCTTTGAGATCCAGACCATGCCCAATGGCAAAACCCGGACCTCCCTCAAGACCATGAGC
 ||||||||||||||||||||||||||||||||||||||||||||||| |||||| |||||  1077
TTCTTTGAGATCCAGACCATGCCCAATGGCAAAACCCGGACCTCCCTTAAGACGATGAGC
Phe

                         369                                     379
ArgArgLysLeuSerGlnGlnLysGluLysLysAlaThrGlnMETLeuAlaIleValLeu
CGTAGGAAGCTCTCCCAGCAGAAGGAGAAGAAAGCCACTCAGATGCTCGCCATTGTTCTC
|| || ||||||||||||||||||||||||||||||||||||||||| ||||||||||||
CGCAGAAAGCTCTCCCAGCAGAAGGAGAAGAAAGCCACTCAGATGCTTGCCATTGTTCTC

             VI          389                                     399
GlyValPheIleIleCysTr0LeuProPhePheIleThrHisIleLeuAsnIleHisCys
▼
GGCGTGTTCATCATCTGCTGGCTGCCCTTCTTCATCACACACATCCTGAACATACACTGT
|| |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||  1197
GCCGTCAACCCCATCATCTACACCACCTTCAACATCGAGTTCCGCAAGGCCTTCATGAAG
                                                   MET
```

FIG. 18G

```
                                    409                                        VII   419
AspCysAsnIleProProValLeuTyrSerAlaPheThrTrpLeuGlyTyrValAsnSer

GACTGCAACATCCCGCCTGTCCTGTACAGCGCCTTCACGTGGCTGGGCTATGTCAACAGC
|| ||||||||||| || ||||| |||||||||||||| |||||||||||||||||||| 
GATTGCAACATCCCACCAGTCCTCTACAGCGCCTTCACATGGCTGGGCTATGTCAACAGT

                           429                            439
AlaValAsnProIleIleTyrThrThrPheAsnIleGluPheArgLysAlaPheLeuLys

GCCGTGAACCCCATCATCTACACCACCTTCAACATTGAGTTCCGCAAGGCCTTCCTGAAG
||||| ||||||||||||||||||||||||||||| |||||||||||||||||| ||||| 1317
GCCGTCAACCCCATCATCTACACCACCTTCAACATCGAGTTCCGCAAGGCCTTCATGAAG
                                                      MET
IleLeuHisCys *

ATCCTCCACTGCTGACTCTGCTGCCTGCCCGCACAGCAGCCTGCTTCCCACCTCCCTGCC
||| | |||||||||
ATCTTGCACTGCTGA
```

FIG. 18H

CAGGCCGGCCAGCCTCACCCTTGCGAACCGTGAGCAGGAAGGCCTGGGTGGATCGGCCTC 1437

CTCTTCTTAGCCCCGGCAGGCCCTGCAGTGTTCGCTTGGCTCCATGCTCCTCACTGCCCG

CACACCCTCACTCTGCCAGGGCAGTGCTAGTGAGCTGGGCATGGTACCAGCCCTGGGGCT 1557

GGCCCCAGCTCAGGGGCAGCTCATAGAGTCCCCCCTCCCACCTCCAGTCCCCCTATCCTT

GGCACCAAAGATGCAGCCGCCTTCCTTGACCTTCCTCTGGGGCTCTAGGGTTGCTGGAGC 1677

CTGAGTCAGGGCCCAGAGGCTGAGTTTTCTCTTTGTGGGGCTTGGCGTGGAGCAGGCGGT

GGGGAGAGATGGACAGTTCACACCCTGCAAGGCCCACAGGAGGCAAGCAAGCTCTCTTGC 1797

CGAGGAGCCAGGCAACTTCAGTCCTGGGAGACCCATGTAAATACCAGACTGCAGGTTGGA

CCCCAAGGATTCCCAAGCCAAAAACCTTAGCTCCCTCCCGCACCCCGATGTGGACCTCTA 1917

FIG. 18I

CTTTCCAGGCTAGTCCGGACCCACCTCACCCCGTTACAGCTCCCCAAGTGGTTTCCACAT

GCTCTGAGAAGAGGAGCCCTCATCTTGAAGGGCCCAGGAGGGTCTATGGGGAGAGGAACT 2037

CCTTGGCCTAGCCCACCCTGCTGCCTTCTGACGGCCCTGCAATGTATCCCTTCTCACAGC

ACATGCTGGCCAGCCTGGGGCCTGGCAGGGAGGTCAGGCCCTGGAACTCTATCTGGGCCT 2157

GGGCTAGGGACATCAGAGGTTCTTTGAGGGACTGCCTCTGCCACACTCTGACGCAAAACC

ACTTTCCTTTTCTATTCCTTCTGGCCTTTCCTCTCTCCTGTTTCCCTTCCCTTCCACTGC 2277

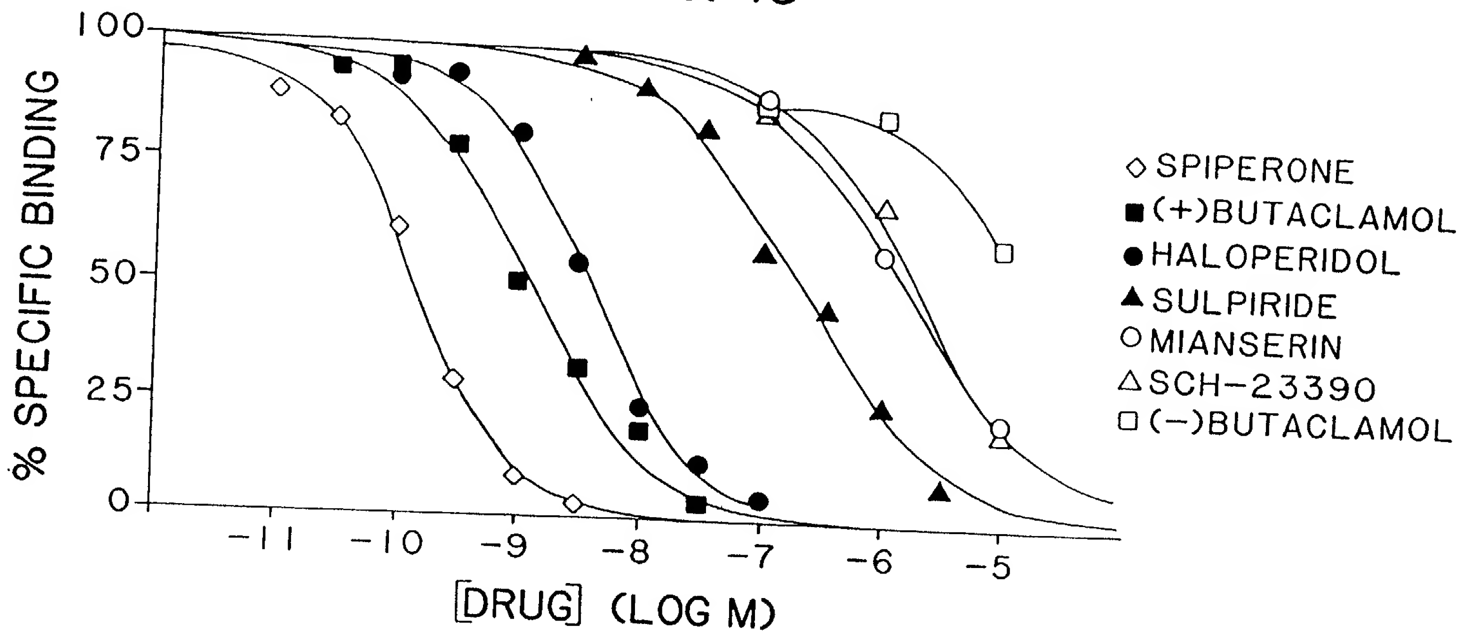
CTCTGCCTTAGAGGAGCCCACGGCTAAGAGGCTGCTGAAAACCATCTGGCCTGGCCTGGC

CCTGCCCTGAGGAAGGAGGGCAAGCTGCAGCTTGGGAGAGCCCCTGGGGCCTAGACTCTG 2397

TAACATCACTATCCGATGCACCAAACTAATAAAACTTTGACGAGTCACCTTC $(A)_n$ 2449

FIG. 18J

FIG. 19


100
75
50
25
0
% SPECIFIC BINDING
-11
-10
-9
-8
-7
-6
-5
[DRUG] (LOG M)
◇ SPIPERONE
■ (+)BUTACLAMOL
● HALOPERIDOL
▲ SULPIRIDE
○ MIANSERIN
△ SCH-23390
□ (-)BUTACLAMOL

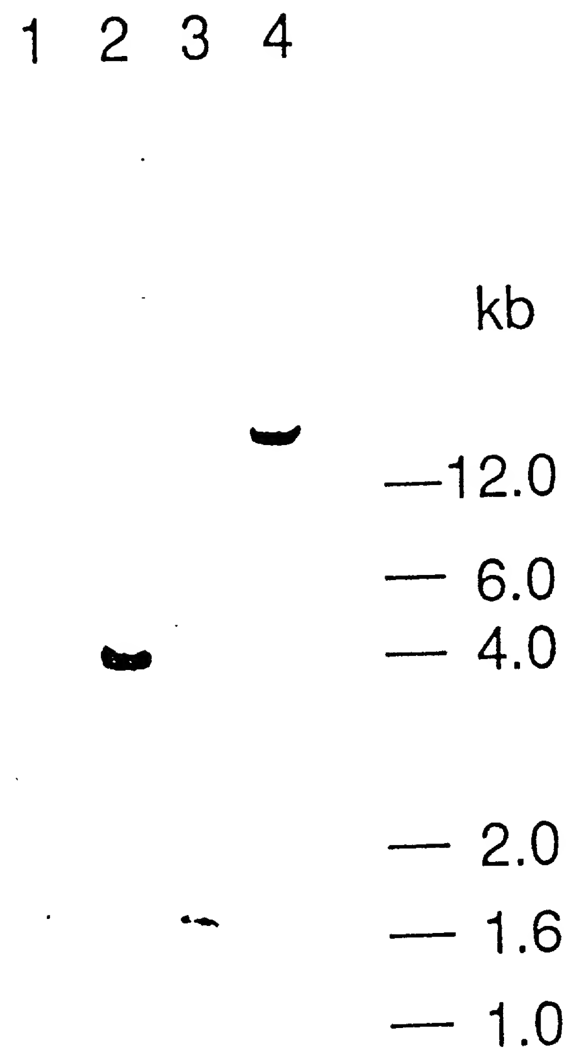
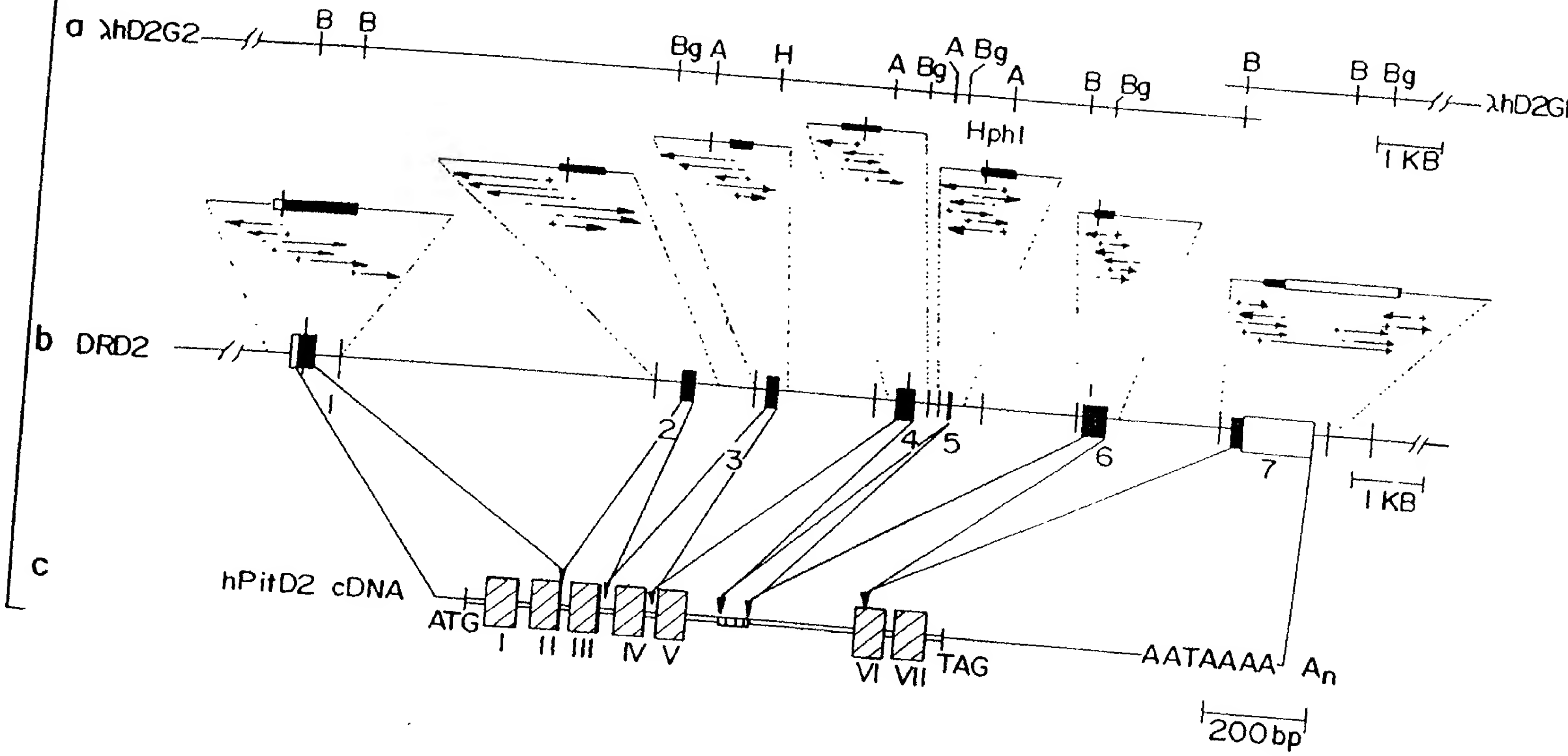


FIG. 20

FIG. 21


a λhD2G2
B
B
Bg
A
H
A
Bg
A
Bg
A
B
Bg
B
B
Bg
λhD2G1
HphI
1 KB
b DRD2
1
2
3
4
5
6
7
1 KB
c
hPitD2 cDNA
ATG
I
II
III
IV
V
VI
VII
TAG
AATAAAA
A_n
200 bp

DRUG	HUMAN D_2	RAT D_2	RAT STRIATUM
SPIPERONE	0.125	0.35	0.56
(+) BUTACLAMOL	0.94	1.2	1.6
HALOPERIDOL	2.4	5.1	5.8
SULPIRIDE	206	160	205
MIANSERIN (5-HT)	2685	4300	4600
SCH 23390 (DI)	2145	2500	3300
(+) BUTACLAMOL	>10,000	>10,000	>10,000
Kd [^{3}H] DOMPERIDONE	0.74	0.40	0.40

FIG. 22